

=> d his nofile

(FILE 'HOME' ENTERED AT 09:54:26 ON 05 SEP 2006)

FILE 'CAPLUS' ENTERED AT 09:54:40 ON 05 SEP 2006

SET LINE 250

SET DETAIL OFF

E US1999-235416/AP,PRN 25

SET LINE LOGIN

SET DETAIL LOGIN

L1 1 SEA ABB=ON US99-235416/PRN
D SCAN

L2 45 SEA ABB=ON SAKOWICZ R?/AU

L3 1091 SEA ABB=ON GOLDSTEIN L?/AU

L4 61 SEA ABB=ON (THERMOMYCES LANUGINOSUS/OBI OR TL/OBI) (W) GAMMA/OBI

E TEST KITS+ALL/CT

L5 17063 SEA ABB=ON TEST KITS/CT

L6 9 SEA ABB=ON (L2 AND L3) OR ((L2 OR L3) AND L4)

L7 1841 SEA ABB=ON KINESINS/CT

L8 2 SEA ABB=ON THERMOMYCES LANUGINOSUS/CT (L) GAMMA/OBI

L9 20619 SEA ABB=ON MICROTUBULE#/OBI

L10 3352 SEA ABB=ON MOTOR/OBI (L) PROTEIN#/OBI

FILE 'REGISTRY' ENTERED AT 09:59:03 ON 05 SEP 2006

E PROTEIN KINASE/CN

L11 1 SEA ABB=ON "PROTEIN KINASE"/CN

FILE 'REGISTRY' ENTERED AT 09:59:23 ON 05 SEP 2006

D IDE

FILE 'CAPLUS' ENTERED AT 09:59:35 ON 05 SEP 2006

L12 97768 SEA ABB=ON L11 OR PROTEIN KINASE#/OBI

L13 0 SEA ABB=ON L8 NOT L4

L14 1 SEA ABB=ON L4 AND (L5 OR L7 OR L9 OR L10 OR L12)

L15 220 SEA ABB=ON L7 AND L9 AND L10

L16 161 SEA ABB=ON L9 (L) L10 AND L7

L17 48 SEA ABB=ON END DIRECT?/OBI

L18 3 SEA ABB=ON L15 AND L17

E SCREENING/CT

L19 42502 SEA ABB=ON L12 (L) (MODULAT?/OBI OR INHIBIT?/OBI OR ACTIVAT?/OBI
)

L20 11 SEA ABB=ON L15 AND L19

L21 0 SEA ABB=ON L16 AND L19

D QUE L20

D SCAN TI L20

L22 1 SEA ABB=ON MAP/TI AND L20

D SCAN

L23 477 SEA ABB=ON L19 (L) ANST/RL

L24 3 SEA ABB=ON L15 AND L23

L25 233 SEA ABB=ON L19 AND L5

D SCA L1

L26 20 SEA ABB=ON L7 AND L25

D QUE

L27 8 SEA ABB=ON L7 AND L25 AND L23

D SCAN TI

FILE 'WPIX' ENTERED AT 10:38:16 ON 05 SEP 2006

L28 36 SEA ABB=ON SAKOWICZ R?/AU

L29 64 SEA ABB=ON GOLDSTEIN L?/AU

L30 1 SEA ABB=ON (THERMOMYCES LANUGINOSUS/BI,ABEX OR TL/BI,ABEX) (A)G
AMMA/BI,ABEX
D TRIAL

L31 3 SEA ABB=ON L28 AND L29
D TRIAL 1-3

L32 252 SEA ABB=ON KINESIN#/BI,ABEX

L33 811 SEA ABB=ON MICROTUBULE#/BI,ABEX OR MICRO TUBULE#/BI,ABEX

L34 120 SEA ABB=ON MOTOR PROTEIN#/BI,ABEX

L35 1863 SEA ABB=ON END DIRECT?/BI,ABEX

L36 4006 SEA ABB=ON PROTEIN KINASE#/BI,ABEX

L37 105 SEA ABB=ON L32 AND (L33 OR L34 OR L35)

L38 54 SEA ABB=ON L32 AND L33 AND L34

L39 3 SEA ABB=ON L32 AND L33 AND L34 AND L35

L40 1 SEA ABB=ON L37 AND L36

L41 2492 SEA ABB=ON L36(3A) (MODULAT?/BI,ABEX OR INHIBIT?/BI,ABEX OR
ACTIVAT?/BI,ABEX)

L42 3 SEA ABB=ON L32 AND L41
D TRIAL 1-3

L43 302435 SEA ABB=ON SCREEN?/BI,ABEX

L44 1372 SEA ABB=ON DRUG#/BI,ABEX (2A) CANDIDATE#/BI,ABEX

L45 484 SEA ABB=ON L41 AND (L43 OR L44)

L46 15 SEA ABB=ON L41 AND L43 AND L44
D TRIAL 1-5
D QUE

L47 45 SEA ABB=ON L41 AND (L33 OR L34 OR L35)

L48 9 SEA ABB=ON L41 AND (L33 OR L34 OR L35) AND (L43 OR L44)
D TRIAL 1-3
D TRIAL L31 1-3

FILE 'STNGUIDE' ENTERED AT 10:52:47 ON 05 SEP 2006

FILE 'WPIX' ENTERED AT 10:58:19 ON 05 SEP 2006

L49 11026 SEA ABB=ON L43(2A) (DRUG#/BI,ABEX OR COMPOUND#/BI,ABEX)

L50 2 SEA ABB=ON L41 AND (L33 OR L34 OR L35) AND (L44 OR L49)
D TRIAL 1-2
D KWIC 1-2

L51 38 SEA ABB=ON L41(S) ((L44 OR L49))

L52 19 SEA ABB=ON L41(10A) ((L44 OR L49))

L53 15 SEA ABB=ON L41(5A) ((L44 OR L49))

L54 0 SEA ABB=ON L51 AND (L33 OR L34 OR L35)

FILE 'STNGUIDE' ENTERED AT 11:01:44 ON 05 SEP 2006

FILE 'WPIX' ENTERED AT 11:02:37 ON 05 SEP 2006

L55 50839 SEA ABB=ON ASSAY#/BI,ABEX

L56 3543 SEA ABB=ON L43(3A) L55

L57 26 SEA ABB=ON L56 AND (L49 OR L44) AND L41

L58 1 SEA ABB=ON L57 AND (L33 OR L34 OR L35)

L59 2 SEA ABB=ON L56 (S) (L49 OR L44) (S) L41

INDEX '1MOBILITY, 2MOBILITY, ABI-INFORM, ADISCTI, AEROSPACE, AGRICOLA,
ALUMINIUM, ANABSTR, ANTE, APOLLIT, AQUALINE, AQUASCI, AQUIRE, BABS,
BIBLIODATA, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA,
CAOLD, CAPLUS, CASREACT, CBNB, CEABA-VTB, CERAB, ...' ENTERED AT 11:05:41
ON 05 SEP 2006

SEA (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA

8 FILE AEROSPACE
1 FILE AGRICOLA
11 FILE ANABSTR

1 FILE AQUASCI
3 FILE BIOENG
14 FILE BIOSIS
2 FILE BIOTECHNO
4 FILE CABA
1 FILE CAOLD
63 FILE CAPLUS
1 FILE CIVILENG
46 FILE COMPENDEX
2 FILE COMPUSCIENCE
1 FILE CONFSCI
1 FILE DDFU
7 FILE DGENE
5 FILE DISSABS
1 FILE DRUGU
2 FILE EMBAL
16 FILE EMBASE
150 FILE ENERGY
1 FILE ENVIROENG
9 FILE EPFULL
9 FILE ESBIOBASE
2 FILE GBFULL
2 FILE GENBANK
1 FILE GEOREF
3 FILE HEALSAFE
6 FILE IFIPAT
152 FILE INIS
4 FILE INPADOC
176 FILE INSPEC
10 FILE INSPHYS
1 FILE JAPIO
16 FILE JICST-EPLUS
3 FILE LIFESCI
3 FILE MECHENG
11 FILE MEDLINE
6 FILE METADEX
33 FILE NTIS
21 FILE PASCAL
9 FILE PATDPAFULL
12 FILE PCTFULL
5 FILE POLLUAB
58 FILE SCISEARCH
1 FILE SOLIDSTATE
6 FILE TEMA
21 FILE TOXCENTER
1 FILE TULSA
1 FILE ULIDAT
19 FILE USPATFULL
3 FILE USPAT2
1 FILE WPIDS
1 FILE WPINDEX

L60 QUE ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA

FILE 'STNGUIDE' ENTERED AT 11:10:58 ON 05 SEP 2006

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,
ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED
AT 11:15:21 ON 05 SEP 2006

L61 138 SEA ABB=ON SAKOWICZ R?/AU

L62 4782 SEA ABB=ON GOLDSTEIN L?/AU
 L63 147 SEA ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
 L64 13861 SEA ABB=ON KINESIN#
 L65 132140 SEA ABB=ON MICROTUBULE# OR MICRO TUBULE#
 L66 7756 SEA ABB=ON MOTOR PROTEIN#
 L67 2654 SEA ABB=ON END DIRECT?
 L68 40 SEA ABB=ON (L61 AND L62) OR ((L61 OR L62) AND L63)
 L69 22 DUP REM L68 (18 DUPLICATES REMOVED)
 ANSWERS '1-2' FROM FILE DRUGU
 ANSWER '3' FROM FILE PASCAL
 ANSWERS '4-5' FROM FILE BIOTECHNO
 ANSWERS '6-17' FROM FILE BIOSIS
 ANSWER '18' FROM FILE LIFESCI
 ANSWERS '19-20' FROM FILE CONFSCI
 ANSWERS '21-22' FROM FILE SCISEARCH
 L70 567385 SEA ABB=ON PROTEIN KINASE#
 L71 3 SEA ABB=ON L63 AND (L64 OR L65 OR L66 OR L67 OR L70)
 L72 377 SEA ABB=ON L64 AND L65 AND L66 AND L67
 L73 83 SEA ABB=ON L64 AND L65 (5A) L66 (5A) L67
 L74 12 SEA ABB=ON L64 (3A) L65 (3A) L66 (3A) L67
 L75 20 SEA ABB=ON L64 (5A) L65 (5A) L66 (5A) L67
 L76 262577 SEA ABB=ON L70 (3A) ((MODULAT? OR INHIBIT? OR ACTIVAT?))
 L77 2376 SEA ABB=ON (SCREEN? OR CANDIDATE#) (3A) (DRUG# OR COMPOUND#) (5A)
 ASSAY?
 L78 0 SEA ABB=ON L76 (S) L77 AND (L64 OR L65 OR L66 OR L67)
 L79 12 SEA ABB=ON L76 (S) L77

 FILE 'MEDLINE' ENTERED AT 11:23:32 ON 05 SEP 2006
 L80 13 SEA ABB=ON SAKOWICZ R?/AU
 L81 1168 SEA ABB=ON GOLDSTEIN L?/AU
 L82 11 SEA ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
 L83 4 SEA ABB=ON (L80 AND L81) OR ((L80 OR L81) AND L82)
 D TRIAL 1-4
 E KINESIN+ALL/CT
 L84 2094 SEA ABB=ON KINESIN/CT
 E MICROTUBULES+ALL/CT
 L85 17967 SEA ABB=ON MICROTUBULES/CT
 L86 76212 SEA ABB=ON ENZYME INHIBITORS/CT
 E MOTOR PROTEIN/CT
 L87 1529 SEA ABB=ON MOTOR PROTEIN#
 L88 359 SEA ABB=ON END DIRECT?
 L89 0 SEA ABB=ON L82 AND (L84 OR L85 OR L86 OR L87 OR L88)
 D TRIAL L82 1-3
 D TRIAL L82 4-11
 L90 325 SEA ABB=ON L84 AND L85 AND (L87 OR L88)
 L91 34 SEA ABB=ON L84 AND L85 AND L87 AND L88
 L92 9 SEA ABB=ON L87 (8A) L88 AND L84 AND L85
 E PROTEIN KINASE/CT
 E E3+ALL
 L93 184405 SEA ABB=ON PROTEIN KINASES+NT/CT
 E SCREENING/CT
 E E4+ALL
 L94 22924 SEA ABB=ON DRUG EVALUATION, PRECLINICAL/CT
 L95 102 SEA ABB=ON L93 AND L94 AND L86
 L96 64 SEA ABB=ON L93/MAJ AND L94 AND L86/MAJ
 L97 13 SEA ABB=ON L93/MAJ AND L94 (L) MT/CT AND L86/MAJ
 D TRIAL 1-4
 L98 28397 SEA ABB=ON L93 (L) AI/CT
 L99 8557 SEA ABB=ON L98/MAJ
 L100 21967 SEA ABB=ON ENZYME ACTIVATION/CT (L) DE/CT

L101 189 SEA ABB=ON L100/MAJ
 L102 19 SEA ABB=ON ((L93/MAJ AND L101) OR L99) AND L94(L)MT/CT
 L103 4668 SEA ABB=ON L94(L)MT/CT
 L104 1977 SEA ABB=ON L103/MAJ
 L105 10 SEA ABB=ON ((L93/MAJ AND L101) OR L99) AND L104
 D TRIAL 1-3
 L106 0 SEA ABB=ON L95 AND L84

FILE 'EMBASE' ENTERED AT 11:33:37 ON 05 SEP 2006

L107 13 SEA ABB=ON SAKOWICZ R?/AU
 L108 922 SEA ABB=ON GOLDSTEIN L?/AU
 L109 16 SEA ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
 L110 5 SEA ABB=ON (L107 AND L108) OR ((L107 OR L108) AND L109)
 D TRIAL 1-5

FILE 'STNGUIDE' ENTERED AT 11:34:20 ON 05 SEP 2006

FILE 'EMBASE' ENTERED AT 12:01:08 ON 05 SEP 2006

L111 5 SEA ABB=ON (L107 AND L108) OR ((L107 OR L108) AND L109)
 D TRIAL 1-5
 L112 2142 SEA ABB=ON KINESIN/CT
 L113 3476 SEA ABB=ON MICROTUBULE ASSEMBLY/CT
 L114 754 SEA ABB=ON MICROTUBULE PROTEIN/CT
 L115 13611 SEA ABB=ON MICROTUBULE/CT
 L116 316 SEA ABB=ON END DIRECT?
 E MOTOR PROTEIN/CT
 E E3+ALL
 L117 569 SEA ABB=ON MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT
 L118 0 SEA ABB=ON L109 AND (L112 OR L113 OR L114 OR L115 OR L116 OR
 L117)
 L119 7 SEA ABB=ON L112 AND (L113 OR L114 OR L115) AND L116 AND L117
 E ENZYME ACTIVAT/CT
 L120 68045 SEA ABB=ON ENZYME ACTIVATION/CT
 L121 1083 SEA ABB=ON ENZYME ACTIVATOR/CT
 E ENZYME MODULAT/CT
 L122 39 SEA ABB=ON ENZYME MODULATION/CT
 L123 16880 SEA ABB=ON ENZYME INHIBITOR/CT
 L124 89209 SEA ABB=ON ENZYME INHIBITION/CT
 E PROTEIN KINASE/CT
 L125 20757 SEA ABB=ON PROTEIN KINASE+NT/CT
 L126 2690 SEA ABB=ON L125/MAJ AND (L120 OR L121 OR L122 OR L123 OR
 L124)
 L127 31 SEA ABB=ON L126 AND (L112 OR L113 OR L114 OR L115 OR L116 OR
 L117 OR L109)
 L128 4 SEA ABB=ON GENERAL REVIEW/DT AND L127
 D TRIAL 1-4
 E ENZYME ACTIVITY/CT
 L129 221084 SEA ABB=ON ENZYME ACTIVITY/CT
 E DRUG SCREENING/CT
 E E3+ALL
 L130 74504 SEA ABB=ON DRUG SCREENING/CT
 E E19+ALL
 L131 22260 SEA ABB=ON SCREENING TEST/CT
 L132 4100 SEA ABB=ON L125/MAJ AND (L120 OR L121 OR L122 OR L123 OR L124
 OR L129)
 L133 24 SEA ABB=ON L132 AND (L130 OR L131)
 D TRIAL 1-4
 L134 4072 SEA ABB=ON PROTEIN KINASE INHIBITOR/CT
 L135 1431 SEA ABB=ON L134/MAJ
 L136 53 SEA ABB=ON L135 AND (L130 OR L131)

L137 71 SEA ABB=ON L133 OR L136
E ANALYTIC METHOD+ALL/CT
D QUE L137
L138 1 SEA ABB=ON L137 AND (L112 OR L113 OR L114 OR L115 OR L116 OR
L117 OR L109)

FILE 'STNGUIDE' ENTERED AT 12:12:41 ON 05 SEP 2006

D QUE L105
D QUE L92
D QUE L79
D QUE L75
D QUE L58
D QUE L59
D QUE L40
D QUE L24
D QUE L27
D QUE L18

FILE 'CAPLUS' ENTERED AT 12:14:47 ON 05 SEP 2006

D QUE L1
D QUE L6

L139 9 SEA ABB=ON L1 OR L6

FILE 'WPIX' ENTERED AT 12:14:49 ON 05 SEP 2006

D QUE L31

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,
ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED
AT 12:14:50 ON 05 SEP 2006

D QUE L68

FILE 'MEDLINE' ENTERED AT 12:14:52 ON 05 SEP 2006

D QUE L83

FILE 'EMBASE' ENTERED AT 12:14:54 ON 05 SEP 2006

D QUE L110

FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, DRUGU, PASCAL, BIOTECHNO, BIOSIS,
ESBIOBASE, LIFESCI, CONFSCI, SCISEARCH' ENTERED AT 12:15:12 ON 05 SEP 2006

L140 26 DUP REM L83 L139 L31 L110 L68 (35 DUPLICATES REMOVED)

ANSWERS '1-4' FROM FILE MEDLINE
ANSWERS '5-10' FROM FILE CAPLUS
ANSWERS '11-21' FROM FILE BIOSIS
ANSWER '22' FROM FILE LIFESCI
ANSWERS '23-24' FROM FILE CONFSCI
ANSWERS '25-26' FROM FILE SCISEARCH
D IBIB ED ABS 1-26

FILE 'STNGUIDE' ENTERED AT 12:15:40 ON 05 SEP 2006

D QUE L14
D QUE L18
D QUE L30
D QUE L39
D QUE L40
D QUE L71
D QUE L75

FILE 'CAPLUS' ENTERED AT 12:17:36 ON 05 SEP 2006

D QUE L14

L141 0 SEA ABB=ON L14 NOT L139

FILE 'WPIX' ENTERED AT 12:17:38 ON 05 SEP 2006
D QUE L30

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,
ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED
AT 12:17:40 ON 05 SEP 2006

D QUE L71

L142 0 SEA ABB=ON L71 NOT L68

FILE 'MEDLINE' ENTERED AT 12:17:48 ON 05 SEP 2006
D QUE L89

FILE 'EMBASE' ENTERED AT 12:17:50 ON 05 SEP 2006
D QUE L118

FILE 'CAPLUS' ENTERED AT 12:19:00 ON 05 SEP 2006
D QUE L14

L143 0 SEA ABB=ON L14 NOT L139

FILE 'WPIX' ENTERED AT 12:19:01 ON 05 SEP 2006
D QUE L30

L144 0 SEA ABB=ON L30 NOT L31

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,
ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED
AT 12:19:04 ON 05 SEP 2006

D QUE L71

L145 0 SEA ABB=ON L71 NOT L68

FILE 'MEDLINE' ENTERED AT 12:19:12 ON 05 SEP 2006
D QUE L89

FILE 'EMBASE' ENTERED AT 12:19:14 ON 05 SEP 2006
D QUE L118

FILE 'STNGUIDE' ENTERED AT 12:19:27 ON 05 SEP 2006

FILE 'CAPLUS' ENTERED AT 12:20:57 ON 05 SEP 2006
D QUE L18

L146 3 SEA ABB=ON L18 NOT L139

FILE 'WPIX' ENTERED AT 12:20:58 ON 05 SEP 2006
D QUE L39

D QUE L40

L147 3 SEA ABB=ON (L39 OR L40) NOT L31

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,
ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED
AT 12:21:01 ON 05 SEP 2006

D QUE L75

L148 20 SEA ABB=ON L75 NOT L68

FILE 'MEDLINE' ENTERED AT 12:21:10 ON 05 SEP 2006
D QUE L92

L149 9 SEA ABB=ON L92 NOT L83

FILE 'EMBASE' ENTERED AT 12:21:12 ON 05 SEP 2006
D QUE L119

L150 7 SEA ABB=ON L119 NOT L110

FILE 'STNGUIDE' ENTERED AT 12:21:21 ON 05 SEP 2006

FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, BIOTECHNO, BIOSIS, ESBIODBASE, LIFESCI, SCISEARCH' ENTERED AT 12:21:44 ON 05 SEP 2006

L151 28 DUP REM L149 L146 L147 L150 L148 (14 DUPLICATES REMOVED)
ANSWERS '1-9' FROM FILE MEDLINE
ANSWERS '10-12' FROM FILE CAPLUS
ANSWERS '13-15' FROM FILE WPIX
ANSWERS '16-21' FROM FILE EMBASE
ANSWERS '22-23' FROM FILE BIOTECHNO
ANSWERS '24-27' FROM FILE BIOSIS
ANSWER '28' FROM FILE LIFESCI
D IALL 1-9
D IBIB ED ABS HITIND 10-12
D IALL ABEQ TECH 13-15
D IALL 16-28

FILE 'STNGUIDE' ENTERED AT 12:22:44 ON 05 SEP 2006

FILE 'CAPLUS' ENTERED AT 12:24:49 ON 05 SEP 2006

D QUE L24
D QUE L27
L152 11 SEA ABB=ON (L24 OR L27) NOT (L18 OR L139)

FILE 'WPIX' ENTERED AT 12:24:50 ON 05 SEP 2006

D QUE L58
D QUE L59
L153 3 SEA ABB=ON (L58 OR L59) NOT (L39 OR L40 OR L31)

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIODBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED AT 12:24:53 ON 05 SEP 2006

D QUE L79
L154 12 SEA ABB=ON L79 NOT (L75 OR L68)

FILE 'MEDLINE' ENTERED AT 12:25:02 ON 05 SEP 2006

D QUE L105
L155 10 SEA ABB=ON L105 NOT (L92 OR L83)

FILE 'EMBASE' ENTERED AT 12:25:03 ON 05 SEP 2006

D QUE L138
L156 1 SEA ABB=ON L138 NOT (L119 OR L110)

FILE 'STNGUIDE' ENTERED AT 12:25:10 ON 05 SEP 2006

FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, DRUGU, PASCAL, BIOTECHNO, ESBIODBASE' ENTERED AT 12:25:33 ON 05 SEP 2006

L157 34 DUP REM L155 L152 L153 L156 L154 (3 DUPLICATES REMOVED)
ANSWERS '1-10' FROM FILE MEDLINE
ANSWERS '11-21' FROM FILE CAPLUS
ANSWERS '22-24' FROM FILE WPIX
ANSWER '25' FROM FILE EMBASE
ANSWERS '26-27' FROM FILE DRUGU
ANSWERS '28-29' FROM FILE BIOTECHNO
ANSWERS '30-34' FROM FILE ESBIODBASE
D IALL 1-10
D IBIB ED ABS HITIND 11-21
D IALL ABEQ TECH 22-24
D IALL 25-34

=> fil reg; d ide
FILE 'REGISTRY' ENTERED AT 09:59:23 ON 05 SEP 2006
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STRUCTURE FILE UPDATES: 4 SEP 2006 HIGHEST RN 905816-92-4
DICTIONARY FILE UPDATES: 4 SEP 2006 HIGHEST RN 905816-92-4

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<http://www.cas.org/ONLINE/UG/regprops.html>

L11 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2006 ACS on STN
RN 372092-80-3 REGISTRY
ED Entered STN: 28 Nov 2001
CN Kinase (phosphorylating), protein (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Neurokinase
CN Protein kinase
MF Unspecified
CI MAN
SR CA
LC STN Files: BIOSIS, CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
1917 REFERENCES IN FILE CA (1907 TO DATE)
17 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
1930 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> =>

=>
=> fil capl; d que l1; d que l6
FILE 'CAPLUS' ENTERED AT 12:14:47 ON 05 SEP 2006
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FILE LAST UPDATED: 4 Sep 2006 (20060904/ED)

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<http://www.cas.org/infopolicy.html>
'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

*Inventor
search*

L1 1 SEA FILE=CAPLUS ABB=ON US99-235416/PRN

L2 45 SEA FILE=CAPLUS ABB=ON SAKOWICZ R?/AU
L3 1091 SEA FILE=CAPLUS ABB=ON GOLDSTEIN L?/AU
L4 61 SEA FILE=CAPLUS ABB=ON (THERMOMYCES LANUGINOSUS/OBI OR
TL/OBI) (W) GAMMA/OBI
L6 9 SEA FILE=CAPLUS ABB=ON (L2 AND L3) OR ((L2 OR L3) AND L4)

=> s l1 or l6

L139 9 L1 OR L6

=> fil wpix; d que l31

FILE 'WPIX' ENTERED AT 12:14:49 ON 05 SEP 2006
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FILE LAST UPDATED: 1 SEP 2006 <20060901/UP>
MOST RECENT DERWENT UPDATE: 200656 <200656/DW>
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'BI ABEX' IS DEFAULT SEARCH FIELD FOR 'WPIX' FILE

L28 36 SEA FILE=WPIX ABB=ON SAKOWICZ R?/AU
L29 64 SEA FILE=WPIX ABB=ON GOLDSTEIN L?/AU
L31 3 SEA FILE=WPIX ABB=ON L28 AND L29

=> fil DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,ESBIOBASE,
LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH

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=> d que 168

L61 138 SEA SAKOWICZ R?/AU
L62 4782 SEA GOLDSTEIN L?/AU
L63 147 SEA (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
L68 40 SEA (L61 AND L62) OR ((L61 OR L62) AND L63)

=> fil medl; d que 183

FILE 'MEDLINE' ENTERED AT 12:14:52 ON 05 SEP 2006

FILE LAST UPDATED: 2 Sep 2006 (20060902/UP). FILE COVERS 1950 TO DATE.

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 is now (26 Feb.) available. For details
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See also:

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http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate
substance identification.

L80 13 SEA FILE=MEDLINE ABB=ON SAKOWICZ R?/AU
L81 1168 SEA FILE=MEDLINE ABB=ON GOLDSTEIN L?/AU
L82 11 SEA FILE=MEDLINE ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMM
A
L83 4 SEA FILE=MEDLINE ABB=ON (L80 AND L81) OR ((L80 OR L81) AND
L82)

=> fil embase; d que 1110

FILE 'EMBASE' ENTERED AT 12:14:54 ON 05 SEP 2006
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FILE COVERS 1974 TO 5 Sep 2006 (20060905/ED)

EMBASE has been reloaded. Enter HELP RLOAD for details.

EMBASE is now updated daily. SDI frequency remains weekly (default)
and biweekly.

This file contains CAS Registry Numbers for easy and accurate
substance identification.

L107 13 SEA FILE=EMBASE ABB=ON SAKOWICZ R?/AU
L108 922 SEA FILE=EMBASE ABB=ON GOLDSTEIN L?/AU
L109 16 SEA FILE=EMBASE ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA

L110 5 SEA FILE=EMBASE ABB=ON (L107 AND L108) OR ((L107 OR L108) AND
L109)

=> dup rem l83,l139,l31,l110,l68

FILE 'MEDLINE' ENTERED AT 12:15:12 ON 05 SEP 2006

FILE 'CAPLUS' ENTERED AT 12:15:12 ON 05 SEP 2006

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PROCESSING COMPLETED FOR L83

PROCESSING COMPLETED FOR L139

PROCESSING COMPLETED FOR L31

PROCESSING COMPLETED FOR L110

PROCESSING COMPLETED FOR L68

L140 26 DUP REM L83 L139 L31 L110 L68 (35 DUPLICATES REMOVED)

ANSWERS '1-4' FROM FILE MEDLINE

ANSWERS '5-10' FROM FILE CAPLUS

ANSWERS '11-21' FROM FILE BIOSIS

ANSWER '22' FROM FILE LIFESCI

ANSWERS '23-24' FROM FILE CONFSCI
ANSWERS '25-26' FROM FILE SCISEARCH

=> d ibib ed abs 1-26

L140 ANSWER 1 OF 26 MEDLINE on STN DUPLICATE 5
ACCESSION NUMBER: 2000095847 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10631986
TITLE: Cloning and expression of kinesins from the thermophilic fungus *Thermomyces lanuginosus*.
AUTHOR: Sakowicz R; Farlow S; Goldstein L S
CORPORATE SOURCE: Howard Hughes Medical Institute, Department of Cellular and Molecular Medicine, School of Medicine, University of California, San Diego, La Jolla 92093-0683, USA.
CONTRACT NUMBER: GM35252 (NIGMS)
SOURCE: Protein science : a publication of the Protein Society, (1999 Dec) Vol. 8, No. 12, pp. 2705-10.
Journal code: 9211750. ISSN: 0961-8368.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 29 Feb 2000
Last Updated on STN: 29 Feb 2000
Entered Medline: 14 Feb 2000
ED Entered STN: 29 Feb 2000
Last Updated on STN: 29 Feb 2000
Entered Medline: 14 Feb 2000
AB The motor domain regions of three novel members of the kinesin superfamily TLKIF1, TLKIFC, and TLBIMC were identified in a thermophilic fungus *Thermomyces lanuginosus*. Based on sequence similarity, they were classified as members of the known kinesin families Unc104/KIF1, KAR3, and BIMC. TLKIF1 was subsequently expressed in *Escherichia coli*. The expression level was high, and the protein was mostly soluble, easy to purify, and enzymatically active. TLKIF1 is a monomeric kinesin motor, which in a gliding motility assay displays a robust plus-directed microtubule movement up to 2 microm/s. The discovery of TLKIF1 also demonstrates that a family of kinesin motors not previously found in fungi may in fact be used in this group of organisms.

L140 ANSWER 2 OF 26 MEDLINE on STN DUPLICATE 7
ACCESSION NUMBER: 1998202613 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9535660
TITLE: A marine natural product inhibitor of kinesin motors.
AUTHOR: Sakowicz R; Berdelis M S; Ray K; Blackburn C L; Hopmann C; Faulkner D J; Goldstein L S
CORPORATE SOURCE: Department of Pharmacology, Division of Cellular and Molecular Medicine, Howard Hughes Medical Institute, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0683, USA.
SOURCE: Science, (1998 Apr 10) Vol. 280, No. 5361, pp. 292-5.
Journal code: 0404511. ISSN: 0036-8075.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 7 May 1998
Last Updated on STN: 7 May 1998

Entered Medline: 28 Apr 1998

ED Entered STN: 7 May 1998

Last Updated on STN: 7 May 1998

Entered Medline: 28 Apr 1998

AB Members of the kinesin superfamily of motor proteins are essential for mitotic and meiotic spindle organization, chromosome segregation, organelle and vesicle transport, and many other processes that require microtubule-based transport. A compound, adociasulfate-2, was isolated from a marine sponge, Haliclona (also known as Adocia) species, that inhibited kinesin activity by targeting its motor domain and mimicking the activity of the microtubule. Thus, the kinesin-microtubule interaction site could be a useful target for small molecule modulators, and adociasulfate-2 should serve as an archetype for specific inhibitors of kinesin functions.

L140 ANSWER 3 OF 26

MEDLINE on STN

DUPLICATE 9

ACCESSION NUMBER: 1998028574 MEDLINE

DOCUMENT NUMBER: PubMed ID: 9363944

TITLE: CENP-E is a plus end-directed kinetochore motor required for metaphase chromosome alignment.

AUTHOR: Wood K W; Sakowicz R; Goldstein L S; Cleveland D W

CORPORATE SOURCE: Laboratory of Cell Biology, Ludwig Institute for Cancer Research, University of California at San Diego, La Jolla 92093-0660, USA.

SOURCE: Cell, (1997 Oct 31) Vol. 91, No. 3, pp. 357-66.
Journal code: 0413066. ISSN: 0092-8674.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF027728

ENTRY MONTH: 199712

ENTRY DATE: Entered STN: 9 Jan 1998

Last Updated on STN: 9 Jan 1998

Entered Medline: 10 Dec 1997

ED Entered STN: 9 Jan 1998

Last Updated on STN: 9 Jan 1998

Entered Medline: 10 Dec 1997

AB Mitosis requires dynamic attachment of chromosomes to spindle microtubules. This interaction is mediated largely by kinetochores. During prometaphase, forces exerted at kinetochores, in combination with polar ejection forces, drive congression of chromosomes to the metaphase plate. A major question has been whether kinetochore-associated microtubule motors play an important role in congression. Using immunodepletion from and antibody addition to Xenopus egg extracts, we show that the kinetochore-associated kinesin-like motor protein CENP-E is essential for positioning chromosomes at the metaphase plate. We further demonstrate that CENP-E powers movement toward microtubule plus ends in vitro. These findings support a model in which CENP-E functions in congression to tether kinetochores to dynamic microtubule plus ends.

L140 ANSWER 4 OF 26

MEDLINE on STN

ACCESSION NUMBER: 96196874 MEDLINE

DOCUMENT NUMBER: PubMed ID: 8612068

TITLE: The muscle in kinesin.

AUTHOR: Sakowicz R; Goldstein L S

SOURCE: Nature structural biology, (1996 May) Vol. 3, No. 5, pp. 404-7.

Journal code: 9421566. ISSN: 1072-8368.

PUB. COUNTRY: United States
 DOCUMENT TYPE: News Announcement
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199606
 ENTRY DATE: Entered STN: 13 Jun 1996
 Last Updated on STN: 13 Jun 1996
 Entered Medline: 3 Jun 1996

ED Entered STN: 13 Jun 1996
 Last Updated on STN: 13 Jun 1996
 Entered Medline: 3 Jun 1996

L140 ANSWER 5 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1

ACCESSION NUMBER: 1999:487304 CAPLUS
 DOCUMENT NUMBER: 131:112405
 TITLE: Identification and expression of the microtubule motor protein kinesin TL- γ
 INVENTOR(S): Sakowicz, Roman; Goldstein, Lawrence S. B.
 PATENT ASSIGNEE(S): The Regents of the University of California, USA
 SOURCE: PCT Int. Appl., 75 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9937659	A1	19990729	WO 1999-US1355	19990122
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9924648	A1	19990809	AU 1999-24648	19990122
US 6723840	B1	20040420	US 2000-724586	20001128 <--
US 6815169	B1	20041109	US 2000-724666	20001128 <--
US 6764830	B1	20040720	US 2000-600823	20001221 <--
PRIORITY APPLN. INFO.:			US 1998-72361P	A2 19980123
			US 1999-235416	A3 19990122 <--
			WO 1999-US1355	W 19990122

ED Entered STN: 06 Aug 1999

AB The invention concerns the isolation of a nucleic acid sequence from *Thermomyces lanuginosus* that encodes the microtubule motor protein kinesin TL- γ with the following properties: the protein's activity includes plus end-directed microtubule motor activity; the protein has a tail domain that has greater than 60% amino acid sequence identity to a TL- γ tail domain as measured using a sequence comparison algorithm; the protein specifically binds to polyclonal antibodies to TL- γ . The invention also concerns antibodies to TL- γ , methods for screening biol. active TL- γ , and kits for screening. Using PCR and degenerate primers, TL- γ was amplified from *Thermomyces lanuginosus* genomic DNA. The nucleic acid sequence was then used as a probe to isolate a longer TL- γ sequence. Recombinant TL- γ was prepared in order to test its activity in a microtubule gliding assay. The

pET23-TL- γ expression vector was constructed and expressed in E. coli. The kinesin TL- γ protein was isolated, it was very stable retaining 100% activity up to 40° after incubation for 15 min as measured using a microtubule dependent ATPase assay. Freshly prepared protein was used to assay microtubule gliding activity. Taxol stabilized microtubule seeds brightly labeled with rhodamine were prepared by incubating a 1:1 ratio of rhodamine labeled bovine brain tubulin; also unlabeled bovine brain tubulin was incorporated into the assay. Flow chambers prepared were preadsorbed with TL- γ motor protein. A microtubule/ATP mix containing polarity marked microtubules, taxol, MgATP and an oxygen scavenging system was then flowed into the chamber. Movement of microtubules was monitored at room temperature on a fluorescence microscope fitted with oil immersion objective and a CCD. For TL- γ activity measurement, recombinant TL- γ protein was attached to a glass coverslip using non-specific adhesion, and gliding of polarity marked microtubules containing brightly fluorescent rhodamine labeled seeds near their minus ends was recorded by time-lapse digital fluorescence microscopy. Microtubules moved with brightly fluorescent seeds leading, indicating that the immobilized TL- γ protein was moving toward microtubule plus ends. No movement was observed in the absence of TL- γ . This experiment demonstrates that TL- γ has plus-ended microtubule motor activity.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 6 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2

ACCESSION NUMBER: 1999:451195 CAPLUS

DOCUMENT NUMBER: 131:97592

TITLE: Kinesin motor modulators derived from the marine sponge adocia

INVENTOR(S): Goldstein, Lawrence S. B.; Faulkner, David John; Sakowicz, Roman; Berdelis, Michael S.; Blackburn, Christine L.; Hopmann, Cordula

PATENT ASSIGNEE(S): The Regents of the University of California, USA

SOURCE: PCT Int. Appl., 73 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9934806	A1	19990715	WO 1999-US321	19990106
W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
AU 9921071	A1	19990726	AU 1999-21071	19990106
EP 1049475	A1	20001108	EP 1999-901353	19990106
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
US 6207403	B1	20010327	US 1999-226772	19990106
JP 2002500190	T2	20020108	JP 2000-527255	19990106
US 6489134	B1	20021203	US 2000-724609	20001128

US 2003127621	A1	20030710	US 2002-305857	20021127
US 6777200	B2	20040817		
US 2004176625	A1	20040909	US 2004-794757	20040303
PRIORITY APPLN. INFO.:			US 1998-70772P	P 19980108
			US 1999-226772	A3 19990106
			WO 1999-US321	W 19990106
			US 2000-724609	A1 20001128
			US 2002-305857	A1 20021127

OTHER SOURCE(S): MARPAT 131:97592

ED Entered STN: 23 Jul 1999

AB This invention provides novel compds. derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity of a microtubule. The compds. act as potent anti-mitogens and are useful in a wide variety of in vitro and in vivo applications [e.g. in mitigating a variety of pathol. conditions characterized by abnormal cell mitosis].

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 7 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3

ACCESSION NUMBER: 1999:194248 CAPLUS

DOCUMENT NUMBER: 130:233824

TITLE: Plus end-directed microtubule motor protein CENP-E required for Xenopus chromosome congression

INVENTOR(S): Wood, Kenneth W.; Sakowicz, Roman; Goldstein, Lawrence S. B.; Cleveland, Don W.

PATENT ASSIGNEE(S): The Regents of the University of California, USA

SOURCE: PCT Int. Appl., 78 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9913061	A1	19990318	WO 1998-US19231	19980910
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2303484	AA	19990318	CA 1998-2303484	19980910
AU 9893918	A1	19990329	AU 1998-93918	19980910
AU 745385	B2	20020321		
EP 1012249	A1	20000628	EP 1998-947039	19980910
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2001526881	T2	20011225	JP 2000-510850	19980910
US 6645748	B1	20031111	US 1998-150867	19980910
US 7009043	B1	20060307	US 2000-724584	20001128
US 2005191631	A1	20050901	US 2003-650280	20030827
PRIORITY APPLN. INFO.:			US 1997-58645P	P 19970911
			US 1998-150867	A1 19980910
			WO 1998-US19231	W 19980910

ED Entered STN: 25 Mar 1999

AB The invention provides isolated nucleic acid and amino acid sequences of

Xenopus centromere-associated protein-E (XCENP-E), antibodies to XCENP-E, methods of screening for CENP-E modulators using biol. active CENP-E, and kits for screening for CENP-E modulators. The full-length cDNA sequences of XCENP-E encodes a protein of 2954 amino acids with a predicted mol. mass of 340 kDa. XCENP-E is a member of the kinesin superfamily of motor proteins, and consists of a 500-amino acid globular N-terminal domain containing a kinesin-like microtubule motor domain linked to a globular tail domain by a region predicted to form a long, discontinuous α -helical coiled coil. This is the first biol. active CENP-E isolated and, surprisingly and contrary to previous reports, it demonstrates a motor that powers chromosome movement toward microtubule plus ends. Using immunodepletion and antibody addition to Xenopus egg exts., the present invention further demonstrates that CENP-E plays an essential role in congression.

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 8 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 4
ACCESSION NUMBER: 1999:420033 CAPLUS
DOCUMENT NUMBER: 131:211782
TITLE: Adociasulfates 1-6, inhibitors of kinesin motor proteins from the sponge Haliclona (aka Adocia) sp.
AUTHOR(S): Blackburn, Christine L.; Hopmann, Cordula; Sakowicz, Roman; Berdelis, Michael S.; Goldstein, Lawrence S. B.; Faulkner, D. John
CORPORATE SOURCE: Scripps Institution of Oceanography, University of California at San Diego, La Jolla, CA, 92093-0212, USA
SOURCE: Journal of Organic Chemistry (1999), 64(15), 5565-5570
CODEN: JOCEAH; ISSN: 0022-3263
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
ED Entered STN: 08 Jul 1999
GI

* STRUCTURE DIAGRAM TOO LARGE FOR DISPLAY - AVAILABLE VIA OFFLINE PRINT *

AB Adociasulfates 1-6 were isolated from an extract of the Palauan sponge Haliclona (aka Adocia) sp. that inhibited the transport of stabilized microtubules by the motor protein kinesin, which was immobilized on a microscope slide. The structures of adociasulfates 1-6, the relative stereochem. of adociasulfates 1 (I), 2, 5, and 6, and the relative stereochem. of subunits of adociasulfates 3 (II) and 4 were determined by interpretation of spectroscopic data. In a quant. assay that measures ATP hydrolysis by kinesin, adociasulfates 2 and 6 were the most active.

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 9 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 10
ACCESSION NUMBER: 1996:282241 CAPLUS
DOCUMENT NUMBER: 124:310323
TITLE: The muscle in kinesin
AUTHOR(S): Sakowicz, Roman; Goldstein, Lawrence S. B.
CORPORATE SOURCE: Howard Hughes Medical Inst., Univ. California, La Jolla, CA, 92093-0683, USA
SOURCE: Nature Structural Biology (1996), 3(5), 404-407

CODEN: NSBIEW; ISSN: 1072-8368
PUBLISHER: Nature Publishing Co.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
ED Entered STN: 14 May 1996
AB A review, with 41 refs. The first high resolution structures of the kinesin and NCD motor proteins reveal their surprising similarity to myosin but leave open the tantalizing question of what properties eet. the directionality of movement along microtubules.

L140 ANSWER 10 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 11
ACCESSION NUMBER: 1997:151799 CAPLUS
DOCUMENT NUMBER: 126:234999
TITLE: Single molecules solvated in pores of polyacrylamide gels

AUTHOR(S): Dickson, Robert M.; Norris, D. J.; Tzeng, Yih-Ling;
Sakowicz, R.; Goldstein, L. S. B.;
Moerner, W. E.

CORPORATE SOURCE: Department Chemistry Biochemistry, University
California San Diego, La Jolla, CA, 92093-0340, USA
SOURCE: Molecular Crystals and Liquid Crystals Science and
Technology, Section A: Molecular Crystals and Liquid
Crystals (1996), 291, 31-39
CODEN: MCLCE9; ISSN: 1058-725X

PUBLISHER: Gordon & Breach
DOCUMENT TYPE: Journal
LANGUAGE: English

ED Entered STN: 08 Mar 1997
AB Individual fluorescent mols. and individual singly-labeled proteins have been observed in the water-filled pores of poly(acrylamide) gels with far-field microscopy. The mol. range of motion is dramatically reduced by the gel framework, thus allowing single mols. to be studied in an aqueous environment for long periods of time. For the small fluorophores, the gel restricts Brownian motion by approx. two orders of magnitude in each direction, thus greatly enhancing the mol.'s detectability. In contrast to dry polymeric hosts, the gel is composed primarily of water and the majority of mols. remain in solution, thus making these gels an ideal medium in which to utilize single mol. detection methods for the study of biol. systems in vitro.

L140 ANSWER 11 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on
STN DUPLICATE 6

ACCESSION NUMBER: 1999:185585 BIOSIS
DOCUMENT NUMBER: PREV199900185585
TITLE: Single-molecule studies of fluorescent proteins and enzymes.

AUTHOR(S): Moerner, W. E. [Reprint author]; Peterman, E. J.; Sosa, H.;
Brasselet, S.; Dickson, R. M.; Kummer, S.; Sakowicz,
R.; Goldstein, L. S. B.

CORPORATE SOURCE: Department of Chemistry, Stanford University, Stanford, CA,
USA

SOURCE: Biophysical Journal, (Jan., 1999) Vol. 76, No. 1 PART 2,
pp. A20. print.
Meeting Info.: Forty-third Annual Meeting of the
Biophysical Society. Baltimore, Maryland, USA. February
13-17, 1999.

CODEN: BIOJAU. ISSN: 0006-3495.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English

ENTRY DATE: Entered STN: 5 May 1999
Last Updated on STN: 5 May 1999
ED Entered STN: 5 May 1999
Last Updated on STN: 5 May 1999

L140 ANSWER 12 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on
STN DUPLICATE 8

ACCESSION NUMBER: 1999:15470 BIOSIS
DOCUMENT NUMBER: PREV199900015470
TITLE: Study of the orientation of kinesin motors bound to
microtubules using single molecule fluorescence
polarization spectroscopy.
AUTHOR(S): Sosa, H. [Reprint author]; Peterman, E. J. G.; Dickson, R.
M.; Sakowicz, R.; Moerner, W. E.; Goldstein,
L. G.
CORPORATE SOURCE: Dep. Pharmacology, Univ. Calif., San Diego, CA 92093, USA
SOURCE: Molecular Biology of the Cell, (Nov., 1998) Vol. 9, No.
SUPPL., pp. 28A. print.
Meeting Info.: 38th Annual Meeting of the American Society
for Cell Biology. San Francisco, California, USA. December
12-16, 1998. American Society for Cell Biology.
CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 20 Jan 1999
Last Updated on STN: 20 Jan 1999
ED Entered STN: 20 Jan 1999
Last Updated on STN: 20 Jan 1999

L140 ANSWER 13 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on
STN

ACCESSION NUMBER: 2006:342933 BIOSIS
DOCUMENT NUMBER: PREV200600349154
TITLE: Plus end-directed microtubule motor required for chromosome
congression.
AUTHOR(S): Wood, Kenneth W. [Inventor]; Sakowicz, Roman
[Inventor]; Goldstein, Lawrence S. B. [Inventor];
Cleveland, Don W. [Inventor]
CORPORATE SOURCE: Foster City, CA USA
ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 07009043 20060307
SOURCE: Official Gazette of the United States Patent and Trademark
Office Patents, (MAR 7 2006)
CODEN: OGUPE7. ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 12 Jul 2006
Last Updated on STN: 12 Jul 2006

ED Entered STN: 12 Jul 2006
Last Updated on STN: 12 Jul 2006
AB The invention provides isolated nucleic acid and amino acid sequences of
Xenopus CENP-E (XCENP-E), antibodies to XCENP-E, methods of screening for
CENP-E modulators using biologically active CENP-E, and kits for screening
for CENP-E modulators.

L140 ANSWER 14 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on
STN

ACCESSION NUMBER: 2004:468880 BIOSIS
DOCUMENT NUMBER: PREV200400473914

TITLE: Identification and expression of a novel kinesin motor protein.
AUTHOR(S): Sakowicz, Roman [Inventor, Reprint Author]; Goldstein, Lawrence S. B. [Inventor]
CORPORATE SOURCE: ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 6815169 20041109
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Nov 9 2004) Vol. 1288, No. 2.
<http://www.uspto.gov/web/menu/patdata.html>. e-file.
ISSN: 0098-1133 (ISSN print).
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 9 Dec 2004
Last Updated on STN: 9 Dec 2004
ED Entered STN: 9 Dec 2004
Last Updated on STN: 9 Dec 2004
AB The invention provides isolated nucleic acid and amino acid sequences of **TL-gamma**, antibodies to **TL-gamma**, methods of screening for **TL-gamma** modulators using biologically active **TL-gamma**, and kits for screening for **TL-gamma** modulators.

L140 ANSWER 15 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:376082 BIOSIS
DOCUMENT NUMBER: PREV200400381987
TITLE: Kinesin motor modulators derived from the marine sponge Adocia.
AUTHOR(S): Goldstein, Lawrence S. B. [Inventor, Reprint Author]; Faulkner, David John [Inventor]; Sakowicz, Roman [Inventor]; Berdelis, Michael S. [Inventor]; Blackburn, Christine L. [Inventor]; Hopmann, Cordula [Inventor]
CORPORATE SOURCE: Frankfurt am Main, Germany
ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 6777200 20040817
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Aug 17 2004) Vol. 1285, No. 3.
<http://www.uspto.gov/web/menu/patdata.html>. e-file.
ISSN: 0098-1133 (ISSN print).
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 22 Sep 2004
Last Updated on STN: 22 Sep 2004
ED Entered STN: 22 Sep 2004
Last Updated on STN: 22 Sep 2004
AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity of a microtubule. The compounds act as potent anti-mitogens and are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 16 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:332625 BIOSIS
DOCUMENT NUMBER: PREV200400337426
TITLE: Thermomyces lanuginosus kinesin motor protein and methods of screening for modulators of kinesin proteins.
AUTHOR(S): Sakowicz, Roman [Inventor, Reprint Author]; Goldstein, Lawrence S. B. [Inventor]

CORPORATE SOURCE: ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 6764830 20040720
SOURCE: Official Gazette of the United States Patent and Trademark
Office Patents, (July 20 2004) Vol. 1284, No. 3.
<http://www.uspto.gov/web/menu/patdata.html>. e-file.
ISSN: 0098-1133 (ISSN print).

DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 4 Aug 2004
Last Updated on STN: 4 Aug 2004

ED Entered STN: 4 Aug 2004

Last Updated on STN: 4 Aug 2004

AB The invention provides isolated nucleic acid and amino acid sequences of
TL-gamma, antibodies to **TL-gamma**,
methods of screening for **TL-gamma** modulating using
biologically active **TL-gamma**, and kits for screening
for **TL-gamma** modulators.

L140 ANSWER 17 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on
STN

ACCESSION NUMBER: 2004:7637 BIOSIS

DOCUMENT NUMBER: PREV200400008401

TITLE: Plus end-directed microtubule motor required for chromosome
congression.

AUTHOR(S): Wood, Kenneth W. [Inventor, Reprint Author]; **Sakowicz,**
Roman [Inventor]; **Goldstein, Lawrence S. B.**
[Inventor]; Cleveland, Don W. [Inventor]

CORPORATE SOURCE: Delmar, CA, USA

ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6645748 20031111

SOURCE: Official Gazette of the United States Patent and Trademark
Office Patents, (Nov 11 2003) Vol. 1276, No. 2.
<http://www.uspto.gov/web/menu/patdata.html>. e-file.
ISSN: 0098-1133 (ISSN print).

DOCUMENT TYPE: Patent

LANGUAGE: English

ENTRY DATE: Entered STN: 17 Dec 2003

Last Updated on STN: 17 Dec 2003

ED Entered STN: 17 Dec 2003

Last Updated on STN: 17 Dec 2003

AB The invention provides isolated nucleic acid and amino acid sequences of
Xenopus CENP-E (XCENP-E), antibodies to XCENP-E, methods of screening for
CENP-E modulators using biologically active CENP-E, and kits for screening
for CENP-E modulators.

L140 ANSWER 18 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on
STN

ACCESSION NUMBER: 2003:56963 BIOSIS

DOCUMENT NUMBER: PREV200300056963

TITLE: Kinesin motor modulators derived from the marine sponge
Adocia.

AUTHOR(S): **Goldstein, Lawrence S.B.** [Inventor, Reprint
Author]; Faulkner, David John [Inventor]; **Sakowicz,**
Roman [Inventor]; Berdelis, Michael S. [Inventor];
Blackburn, Christine L. [Inventor]; Hopmann, Cordula
[Inventor]

CORPORATE SOURCE: San Diego, CA, USA

ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6489134 20021203

SOURCE: Official Gazette of the United States Patent and Trademark

Office Patents, (Dec 3 2002) Vol. 1265, No. 1.
<http://www.uspto.gov/web/menu/patdata.html>. e-file.
ISSN: 0098-1133 (ISSN print).

DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 22 Jan 2003
Last Updated on STN: 22 Jan 2003

ED Entered STN: 22 Jan 2003

Last Updated on STN: 22 Jan 2003

AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity of a microtubule. The compounds act as potent anti-mitogens and are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 19 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2001:461909 BIOSIS

DOCUMENT NUMBER: PREV200100461909

TITLE: Kinesin motor modulators derived from the marine sponge Adocia.

AUTHOR(S): Goldstein, Lawrence S. B. [Inventor, Reprint author]; Faulkner, David John [Inventor]; Sakowicz, Roman [Inventor]; Berdelis, Michael S. [Inventor]; Blackburn, Christine L. [Inventor]; Hopmann, Cordula [Inventor]

CORPORATE SOURCE: San Diego, CA, USA

ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6207403 20010327

SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Mar. 27, 2001) Vol. 1244, No. 4. e-file.
CODEN: OGUPE7. ISSN: 0098-1133.

DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Oct 2001
Last Updated on STN: 22 Feb 2002

ED Entered STN: 3 Oct 2001

Last Updated on STN: 22 Feb 2002

AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity of a microtubule. The compounds act as potent anti-mitogens and are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 20 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 1998:20152 BIOSIS

DOCUMENT NUMBER: PREV199800020152

TITLE: CENP-E is a plus end-directed kinetochore motor required for chromosome congression.

AUTHOR(S): Wood, K. W. [Reprint author]; Sakowicz, R.; Goldstein, L. S. B.; Cleveland, D. W. [Reprint author]

CORPORATE SOURCE: Lab. Cell Biol., Ludwig Inst. Cancer Research, La Jolla, CA 92093-0660, USA

SOURCE: Molecular Biology of the Cell, (Nov., 1997) Vol. 8, No. SUPPL., pp. 125A. print.
Meeting Info.: 37th Annual Meeting of the American Society for Cell Biology. Washington, D.C., USA. December 13-17, 1997. American Society for Cell Biology.

CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 5 Jan 1998
Last Updated on STN: 5 Jan 1998
ED Entered STN: 5 Jan 1998
Last Updated on STN: 5 Jan 1998

L140 ANSWER 21 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 1997:95559 BIOSIS
DOCUMENT NUMBER: PREV199799394762
TITLE: Cloning, expression, and purification of kinesin superfamily members from the thermophilic fungus.
AUTHOR(S): Sakowicz, R.; Farlow, S.; Goldstein, L. S. B.
CORPORATE SOURCE: Howard Hughes Med. Inst., Div. Cell. Mol. Med., Dep. Pharmacol., Univ. Calif. San Diego, 9500 Gilman Dr., La Jolla, CA 92093-0683, USA
SOURCE: Molecular Biology of the Cell, (1996) Vol. 7, No. SUPPL., pp. 215A.
Meeting Info.: Annual Meeting of the 6th International Congress on Cell Biology and the 36th American Society for Cell Biology. San Francisco, California, USA. December 7-11, 1996.
CODEN: MBCEEV. ISSN: 1059-1524.
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
Conference; (Meeting Poster)
LANGUAGE: English
ENTRY DATE: Entered STN: 3 Mar 1997
Last Updated on STN: 3 Mar 1997
ED Entered STN: 3 Mar 1997
Last Updated on STN: 3 Mar 1997

L140 ANSWER 22 OF 26 LIFESCI COPYRIGHT 2006 CSA on STN

ACCESSION NUMBER: 2003:77194 LIFESCI
TITLE: Kinesin motor modulators derived from the marine sponge Adocia
AUTHOR: Goldstein, L.S.B.; Faulkner, D.J.; Sakowicz, R.; Berdelis, M.S.; Blackburn, C.L.; Hopmann, C.
CORPORATE SOURCE: The Regents of the University of California, Oakland, California
SOURCE: (20021203) . US Patent: 6489134; US CLASS: 435/21; 435/6; 514/172; 514/182; 514/518; 585/350.
DOCUMENT TYPE: Patent
FILE SEGMENT: Q4
LANGUAGE: English
SUMMARY LANGUAGE: English

AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity of a microtubule. The compounds act as potent anti-mitogens and are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 23 OF 26 CONFSCI COPYRIGHT 2006 CSA on STN

ACCESSION NUMBER: 1999:35078 CONFSCI
DOCUMENT NUMBER: 99-047572
TITLE: Single-molecule studies of fluorescent proteins and

enzymes. Topic(s): 09A 01D
AUTHOR: Moerner, W.E.; Peterman, E.J.; Sosa, H.; Brasselet, S.;
Dickson, R.M.; Kummer, S.; Sakowicz, R.;
Goldstein, L.S.B.
CORPORATE SOURCE: Stanford Univ., USA
SOURCE: Biophysical Society, 9650 Rockville Pike, Bethesda, MD
20814, USA; phone: (301) 530-7114; fax: (301) 530-7133;
email: society@biophysics.faseb.org; URL:
www.biophysics.faseb.org, Abstracts available. Price \$25..
Meeting Info.: 991 0048: 43rd Annual Meeting of the
Biophysical Society (9910048). Baltimore, MD (USA). 13-17
Feb 1999. Biophysical Society.
DOCUMENT TYPE: Conference
FILE SEGMENT: DCCP
LANGUAGE: English

L140 ANSWER 24 OF 26 CONFSCI COPYRIGHT 2006 CSA on STN
ACCESSION NUMBER: 1999:26143 CONFSCI
DOCUMENT NUMBER: 99-038637
TITLE: Study of the orientation of kinesin motors bound to
microtubules using single molecule fluorescence
polarization spectroscopy
AUTHOR: Sosa, H.; Peterman, E.J.G.; Dickson, R.M.; Sakowicz,
R.; Moerner, W.E.; Goldstein, L.G.
CORPORATE SOURCE: Dep. Pharmacol., Univ. California at San Diego, CA 92093,
USA
SOURCE: American Society for Cell Biology, 9650 Rockville Pike,
Bethesda, MD 20814, USA; phone: (301) 530-7153; fax: (301)
530-7139; email: ascbinfo@ascb.org; URL:
www.ascb.org/ascb/, Abstracts available. Price \$45. Paper
No. 159.
Meeting Info.: 984 0478: 38th American Society for Cell
Biology Annual Meeting (9840478). San Francisco, CA (USA).
12-16 Dec 1998. ASCB, Bio-Rad, Genentech, Jeol USA, Johnson
& Johnson, Leica, Leadership Alliance, Mark-Rambar Family
Foundation.
DOCUMENT TYPE: Conference
FILE SEGMENT: DCCP
LANGUAGE: English

L140 ANSWER 25 OF 26 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on
STN
ACCESSION NUMBER: 1997:848661 SCISEARCH
THE GENUINE ARTICLE: YF096
TITLE: CENP-E is a plus end-directed kinetochore motor required
for chromosome congression
AUTHOR: Wood K W (Reprint); Sakowicz R; Goldstein L
S B; Cleveland D W
CORPORATE SOURCE: UNIV CALIF SAN DIEGO, CELL BIOL LAB, LUDWIG INST CANC RES,
LA JOLLA, CA 92093; UNIV CALIF SAN DIEGO, HOWARD HUGHES
MED INST, DIV CELLULAR & MOL MED, LA JOLLA, CA 92093
COUNTRY OF AUTHOR: USA
SOURCE: MOLECULAR BIOLOGY OF THE CELL, (NOV 1997) Vol. 8, Supp.
[S], pp. 723-723.
ISSN: 1059-1524.
PUBLISHER: AMER SOC CELL BIOLOGY, 8120 WOODMONT AVE, STE 750,
BETHESDA, MD 20814-2755 USA.
DOCUMENT TYPE: Conference; Journal
LANGUAGE: English
REFERENCE COUNT: 0

ENTRY DATE: Entered STN: 1997
Last Updated on STN: 1997

ED Entered STN: 1997
Last Updated on STN: 1997

L140 ANSWER 26 OF 26 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on
STN

ACCESSION NUMBER: 1997:46229 SCISEARCH

THE GENUINE ARTICLE: WB018

TITLE: Cloning, expression, and purification of kinesin
superfamily members from the thermophilic fungus.

AUTHOR: Sakowicz R (Reprint); Farlow S; Goldstein L
S B

CORPORATE SOURCE: UNIV CALIF SAN DIEGO, DEPT PHARMACOL, DIV CELLULAR & MOL
MED, HOWARD HUGHES MED INST, LA JOLLA, CA 92093

COUNTRY OF AUTHOR: USA

SOURCE: MOLECULAR BIOLOGY OF THE CELL, (DEC 1996) Vol. 7, Supp.
[S], pp. 1250-1250.
ISSN: 1059-1524.

PUBLISHER: AMER SOC CELL BIOLOGY, 8120 WOODMONT AVE, STE 750,
BETHESDA, MD 20814-2755 USA.

DOCUMENT TYPE: Conference; Journal

LANGUAGE: English

REFERENCE COUNT: 0

ENTRY DATE: Entered STN: 1997
Last Updated on STN: 1997

ED Entered STN: 1997
Last Updated on STN: 1997

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L7 1841 SEA FILE=CAPLUS ABB=ON KINESINS/CT
L9 20619 SEA FILE=CAPLUS ABB=ON MICROTUBULE#/OBI
L10 3352 SEA FILE=CAPLUS ABB=ON MOTOR/OBI (L) PROTEIN#/OBI
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L12 97768 SEA FILE=CAPLUS ABB=ON L11 OR PROTEIN KINASE#/OBI
L14 1 SEA FILE=CAPLUS ABB=ON L4 AND (L5 OR L7 OR L9 OR L10 OR L12)

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L143

0 L14 NOT

L139

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L63 147 SEA (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
L64 13861 SEA KINESIN#
L65 132140 SEA MICROTUBULE# OR MICRO TUBULE#
L66 7756 SEA MOTOR PROTEIN#
L67 2654 SEA END DIRECT?
L70 567385 SEA PROTEIN KINASE#
L71 3 SEA L63 AND (L64 OR L65 OR L66 OR L67 OR L70)

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L145

0 L71 NOT L68

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FILE 'MEDLINE' ENTERED AT 12:19:12 ON 05 SEP 2006

FILE LAST UPDATED: 2 Sep 2006 (20060902/UP). FILE COVERS 1950 TO DATE.

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A
L84 2094 SEA FILE=MEDLINE ABB=ON KINESIN/CT
L85 17967 SEA FILE=MEDLINE ABB=ON MICROTUBULES/CT
L86 76212 SEA FILE=MEDLINE ABB=ON ENZYME INHIBITORS/CT
L87 1529 SEA FILE=MEDLINE ABB=ON MOTOR PROTEIN#
L88 359 SEA FILE=MEDLINE ABB=ON END DIRECT?
L89 0 SEA FILE=MEDLINE ABB=ON L82 AND (L84 OR L85 OR L86 OR L87 OR
L88)

=> fil embase; d que l118

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substance identification.

L109	16	SEA FILE=EMBASE ABB=ON	(THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
L112	2142	SEA FILE=EMBASE ABB=ON	KINESIN/CT
L113	3476	SEA FILE=EMBASE ABB=ON	MICROTUBULE ASSEMBLY/CT
L114	754	SEA FILE=EMBASE ABB=ON	MICROTUBULE PROTEIN/CT
L115	13611	SEA FILE=EMBASE ABB=ON	MICROTUBULE/CT
L116	316	SEA FILE=EMBASE ABB=ON	END DIRECT?
L117	569	SEA FILE=EMBASE ABB=ON	MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT
L118	0	SEA FILE=EMBASE ABB=ON	L109 AND (L112 OR L113 OR L114 OR L115 OR L116 OR L117)

=>

=> => fil capl; d que l18

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FILE COVERS 1907 - 5 Sep 2006 VOL 145 ISS 11

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'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

L7	1841	SEA	FILE=CAPLUS	ABB=ON	KINESINS/CT
L9	20619	SEA	FILE=CAPLUS	ABB=ON	MICROTUBULE#/OBI
L10	3352	SEA	FILE=CAPLUS	ABB=ON	MOTOR/OBI (L) PROTEIN#/OBI
L15	220	SEA	FILE=CAPLUS	ABB=ON	L7 AND L9 AND L10
L17	48	SEA	FILE=CAPLUS	ABB=ON	END DIRECT?/OBI
L18	3	SEA	FILE=CAPLUS	ABB=ON	L15 AND L17

=> s l18 not l139

L146

3 L18 NOT L139

previously printed

=> fil wpix; d que l39; d que l40

FILE 'WPIX' ENTERED AT 12:20:58 ON 05 SEP 2006

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FILE LAST UPDATED: 1 SEP 2006 <20060901/UP>

MOST RECENT DERWENT UPDATE: 200656 <200656/DW>

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 'BI ABEX' IS DEFAULT SEARCH FIELD FOR 'WPIX' FILE

L32 252 SEA FILE=WPIX ABB=ON KINESIN#/BI,ABEX
 L33 811 SEA FILE=WPIX ABB=ON MICROTUBULE#/BI,ABEX OR MICRO TUBULE#/BI,
 ABEX
 L34 120 SEA FILE=WPIX ABB=ON MOTOR PROTEIN#/BI,ABEX
 L35 1863 SEA FILE=WPIX ABB=ON END DIRECT?/BI,ABEX
 L39 3 SEA FILE=WPIX ABB=ON L32 AND L33 AND L34 AND L35

L32 252 SEA FILE=WPIX ABB=ON KINESIN#/BI,ABEX
 L33 811 SEA FILE=WPIX ABB=ON MICROTUBULE#/BI,ABEX OR MICRO TUBULE#/BI,
 ABEX
 L34 120 SEA FILE=WPIX ABB=ON MOTOR PROTEIN#/BI,ABEX
 L35 1863 SEA FILE=WPIX ABB=ON END DIRECT?/BI,ABEX
 L36 4006 SEA FILE=WPIX ABB=ON PROTEIN KINASE#/BI,ABEX
 L37 105 SEA FILE=WPIX ABB=ON L32 AND (L33 OR L34 OR L35)
 L40 1 SEA FILE=WPIX ABB=ON L37 AND L36

=> s l39,l40 not l31

L147 3 (L39 OR L40) NOT (L31) *previously printed*

=> fil DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,ESBIOBASE,
 LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH

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=> d que 175

L64 13861 SEA KINESIN#
L65 132140 SEA MICROTUBULE# OR MICRO TUBULE#
L66 7756 SEA MOTOR PROTEIN#
L67 2654 SEA END DIRECT?
L75 20 SEA L64 (5A) L65 (5A) L66 (5A) L67

=> s 175 not 168

L148 20 L75 NOT L68

*previously
printed*

=> fil medl; d que 192

FILE 'MEDLINE' ENTERED AT 12:21:10 ON 05 SEP 2006

FILE LAST UPDATED: 2 Sep 2006 (20060902/UP). FILE COVERS 1950 TO DATE.

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 is now (26 Feb.) available. For details on the 2006 reload, enter HELP RLOAD at an arrow prompt (=>).
See also:

<http://www.nlm.nih.gov/mesh/>
http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate substance identification.

L84 2094 SEA FILE=MEDLINE ABB=ON KINESIN/CT
L85 17967 SEA FILE=MEDLINE ABB=ON MICROTUBULES/CT
L87 1529 SEA FILE=MEDLINE ABB=ON MOTOR PROTEIN#

L88 359 SEA FILE=MEDLINE ABB=ON END DIRECT?
L92 9 SEA FILE=MEDLINE ABB=ON L87(8A)L88 AND L84 AND L85

=> s 192 not 183

L149

9 L92 NOT L83

*previously
printed*

=> fil embase; d que 1119

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This file contains CAS Registry Numbers for easy and accurate
substance identification.

L112 2142 SEA FILE=EMBASE ABB=ON KINESIN/CT
L113 3476 SEA FILE=EMBASE ABB=ON MICROTUBULE ASSEMBLY/CT
L114 754 SEA FILE=EMBASE ABB=ON MICROTUBULE PROTEIN/CT
L115 13611 SEA FILE=EMBASE ABB=ON MICROTUBULE/CT
L116 316 SEA FILE=EMBASE ABB=ON END DIRECT?
L117 569 SEA FILE=EMBASE ABB=ON MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT

L119 7 SEA FILE=EMBASE ABB=ON L112 AND (L113 OR L114 OR L115) AND
L116 AND L117

=> s 1119 not 1110

L150

7 L119 NOT L110

*previously
printed*

=> => dup rem 1149,1146,1147,1150,1148

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PROCESSING COMPLETED FOR L149

PROCESSING COMPLETED FOR L146

PROCESSING COMPLETED FOR L147

PROCESSING COMPLETED FOR L150

PROCESSING COMPLETED FOR L148

L151 28 DUP REM L149 L146 L147 L150 L148 (14 DUPLICATES REMOVED)

ANSWERS '1-9' FROM FILE MEDLINE

ANSWERS '10-12' FROM FILE CAPLUS

ANSWERS '13-15' FROM FILE WPIX

ANSWERS '16-21' FROM FILE EMBASE

ANSWERS '22-23' FROM FILE BIOTECHNO

ANSWERS '24-27' FROM FILE BIOSIS

ANSWER '28' FROM FILE LIFESCI

=> d iall 1-9; d ibib ed abs hitind 10-12; d iall abeq tech 13-15; d iall 16-28

L151 ANSWER 1 OF 28 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2005237850 MEDLINE
DOCUMENT NUMBER: PubMed ID: 15875026
TITLE: The bipolar mitotic kinesin Eg5 moves on both microtubules that it crosslinks.
AUTHOR: Kapitein Lukas C; Peterman Erwin J G; Kwok Benjamin H; Kim Jeffrey H; Kapoor Tarun M; Schmidt Christoph F
CORPORATE SOURCE: Department of Physics and Astronomy and Laser Centre, Vrije Universiteit, De Boelelaan 1081, 1081 HV Amsterdam, The Netherlands.
SOURCE: Nature, (2005 May 5) Vol. 435, No. 7038, pp. 114-8.
Journal code: 0410462. E-ISSN: 1476-4687.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200505
ENTRY DATE: Entered STN: 6 May 2005
Last Updated on STN: 19 May 2005
Entered Medline: 18 May 2005

ABSTRACT:

During cell division, mitotic spindles are assembled by microtubule-based motor proteins. The bipolar organization of spindles is essential for proper segregation of chromosomes, and requires plus-end-directed homotetrameric motor proteins of the widely conserved kinesin-5 (BimC) family. Hypotheses for bipolar spindle formation include the 'push-pull mitotic muscle' model, in which kinesin-5 and opposing motor proteins act between overlapping microtubules. However, the precise roles of kinesin-5 during this process are unknown. Here we show that the vertebrate kinesin-5 Eg5 drives the sliding of microtubules depending on their relative orientation. We found in controlled in vitro assays that Eg5 has the remarkable capability of simultaneously moving at approximately 20 nm s⁻¹ towards the plus-ends of each of the two microtubules it crosslinks. For anti-parallel microtubules, this results in relative sliding at approximately 40 nm s⁻¹, comparable to spindle pole separation rates in vivo. Furthermore, we found that Eg5 can tether microtubule plus-ends, suggesting an additional

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OM protein - protein search, using sw model

Run on: September 1, 2006, 14:22:02 ; Search time 187.583 Seconds
(without alignments)
1910.930 Million cell updates/sec

Title: US-09-235-416-1
Perfect score: 4030
Sequence: 1 MSGGKIKVVRVRFPPNARE.....ELRQQAQMEALKTAKQER 784

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4030	100.0	784	2	AAV06618
2	1684.5	41.8	1714	8	ABM83648 Thermomyc
3	1684.5	41.8	1721	8	ABM83647 Human dia
4	1679	41.7	1199	8	ABM83671 Human dia
5	1674.5	41.6	1696	8	ABM83653 Human dia
6	1674.5	41.6	1709	8	ABM83649 Human dia
7	1674.5	41.6	1722	8	ABM83646 Human dia
8	1673	41.5	1708	8	ABM83650 Human dia
9	1669.5	41.4	1699	8	ABM83651 Human dia
10	1668.5	41.4	1816	3	AA836227 Human dia
11	1667.5	41.4	1805	7	ADJ95088 Novel NOV
12	1666.5	41.4	1770	6	AAE35317 Mouse KIF
13	1661.5	41.2	1823	5	AB807867 Human kin
14	1660.5	41.2	883	4	AAH40034 Human pol
15	1659.5	41.2	1697	8	ABM83652 Human dia
16	1658	41.1	1103	3	AAV51328 Human KLI
17	1658	41.1	1103	6	AAE04316 Human kin
18	1658	41.1	1103	4	ABG72054 Human kin
19	1658	41.1	1103	7	ADG63388 Human kin
20	1655	40.6	1773	4	AB883908 Drosophila
21	1463.5	36.3	1805	4	ABP68930 Human pol
22	1431.5	35.5	1362	5	AAU74840 Human Hsk
23	1430	35.5	757	4	AAU19569 Human dia

24	1430	35.5	757	5	ABP51294	ABP51294 Human MDD
25	1423	35.3	762	5	ABG60124	ABG60124 Human DIT
26	1413	35.1	1507	8	ADQ97525	ADQ97525 Human can
27	1412	35.0	1826	7	ADJ69671	ADJ69671 Human hea
28	1412	35.0	1826	8	ADL83235	ADL83235 Human PRO
29	1407.5	34.9	1844	8	ADQ97522	ADQ97522 Mouse can
30	1396.5	34.7	1921	4	AB862962	AB862962 Drosophila
31	1386	34.4	1815	8	ADR66952	ADR66952 Human pro
32	1386	34.4	1815	8	ADR66054	ADR66054 Human pro
33	1386	34.4	1815	8	ADR66951	ADR66951 Human pro
34	1386	34.4	1815	8	ADR66053	ADR66053 Human pro
35	1347	33.4	944	7	ADM04401	ADM04401 Human pro
36	1347	33.4	944	9	AEC87331	AEC87331 Human CDN
37	1347	33.4	1317	9	AED07567	AED07567 Chromosom
38	1347	33.4	1392	6	AAE32129	AAE32129 Human cyt
39	1347	33.4	1392	7	ADJ94858	ADJ94858 Novel NOV
40	1347	33.4	1393	8	ADN00367	ADN00367 Novel hum
41	1311.5	32.5	1375	5	AB879531	AB879531 Human kin
42	1311.5	32.5	1375	5	AB884481	AB884481 Human Hsk
43	1311.5	32.5	1375	5	AAE22525	AAE22525 Human Hsk
44	1307	32.4	1394	7	ADJ94856	ADJ94856 Novel NOV
45	1278.5	31.7	504	3	AA863189	AA863189 Gene 5 hu

ALIGNMENTS

RESULT 1
ID AAY06618 standard; protein; 784 AA.
XX
AC AAY06618;
DT 26-OCT-1999 (first entry)
XX
XX Thermomyces lanuginosus kinesin motor protein TL-gamma.
DE
XX TL-gamma; kinesin; motor protein; microtubule; unc-104; infection;
KM neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; amyotrophic lateral sclerosis.
XX
OS Thermomyces lanuginosus.
XX
PN W09937659-A1.
XX
PD 29-JUL-1999.
XX
PF 22-JAN-1999; 99WO-US001355.
XX
PR 23-JAN-1998; 98US-0072361P.
XX
PA (REGC) UNIV CALIFORNIA.
PI Sakowicz R, Goldstein LSB;
XX WPI, 1999-493950/41.
XX N-PSDB; AAX87656.
XX
PT New nucleic acid encoding microtubule motor protein, used for diagnosis
XX of fungal infection and neurodegenerative disease.
XX
PS Claim 5; Page 70-71; 75pp; English.
XX
XX This sequence represents Thermomyces lanuginosus TL-gamma, a novel ATP-
XX dependent, plus end-directed microtubule motor protein that is a member
XX of the unc-104 family and kinesin superfamily. The invention provides TL-
XX gamma nucleic acids (see AAX87656), proteins and antibodies, and methods
XX of screening for TL-gamma modulators potentially useful for treating
XX hyphal fungal infections and diseases caused by mutated TL-gamma, e.g.
XX neurodegeneration involving anterograde axonal transport, such as
XX Alzheimer's, Parkinson's or Huntington's diseases or amyotrophic lateral
XX sclerosis. Detection of TL-gamma allows differentiation between hyphal
XX and non-hyphal fungal infections

```

XX      SQ      Sequence 784 AA;
Query Match      100.0%; Score 4030; DB 2; Length 784;
Best Local Similarity 100.0%; Pred. No. 6.5e-299;
Matches 784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MSGGNIKVYVVRPPNAREIDRGACIYRMESGNOTITLPPGAEKARKSGKTTIDGPK 60
DB      1  MSGGNIKVYVVRPPNAREIDRGACIYRMESGNOTITLPPGAEKARKSGKTTIDGPK 60
QY      61  AFAFPRSYSPFKNAPNARYROEDLFODLGVPLLDNAFKGNNNCIFAYGOTSGSKSYMMG 120
DB      61  AFAFPRSYSPFKNAPNARYROEDLFODLGVPLLDNAFKGNNNCIFAYGOTSGSKSYMMG 120
QY      121 YGKEHGVIPRICODMERRINELQDKNLTCTVEVSYLEIYNERVRLDLPSTKGNLKVRE 180
DB      121 YGKEHGVIPRICODMERRINELQDKNLTCTVEVSYLEIYNERVRLDLPSTKGNLKVRE 180
QY      181 HPSGTPIYVEDLAKLVYRSFOEIEENLMDENGNKARTVAATNMNETSSKSHAVFTLTQKXH 240
DB      181 HPSGTPIYVEDLAKLVYRSFOEIEENLMDENGNKARTVAATNMNETSSKSHAVFTLTQKXH 240
QY      241 DEETKMDTEKVAKISLVDLAGESEATSGATGARLKEGAENRSLSLTGRVIAALADMSS 300
DB      241 DEETKMDTEKVAKISLVDLAGESEATSGATGARLKEGAENRSLSLTGRVIAALADMSS 300
QY      301 GKOKKNQVPRDSVLTWLLKDSLGNSMTAMIAISPADINEETLSTLRVYADSAKRIL 360
DB      301 GKOKKNQVPRDSVLTWLLKDSLGNSMTAMIAISPADINEETLSTLRVYADSAKRIL 360
QY      361 NNAVVEDNNAIMIRELKEELAQBSKLSGSGGGGAGAGSGPVEEYPPDPLEKOIV 420
DB      361 NNAVVEDNNAIMIRELKEELAQBSKLSGSGGGGAGAGSGPVEEYPPDPLEKOIV 420
QY      421 SIOOPDATVKKMSKAEIVQLNQSEKLYRDLNQTEWEKLAKEEIHKEEALBELGISI 480
DB      421 SIOOPDATVKKMSKAEIVQLNQSEKLYRDLNQTEWEKLAKEEIHKEEALBELGISI 480
QY      481 EKGFGPPIYHKSMPHLYNISDDPLAECLVYNIKKPQTVGVANNQTOAEIRLNGSKILK 540
DB      481 EKGFGPPIYHKSMPHLYNISDDPLAECLVYNIKKPQTVGVANNQTOAEIRLNGSKILK 540
QY      541 EHCTEENVNVVTIYVNEKAAVWVNGVRIDKPTRLSGRIILGDPIFRFHPNPEBARAE 600
DB      541 EHCTEENVNVVTIYVNEKAAVWVNGVRIDKPTRLSGRIILGDPIFRFHPNPEBARAE 600
QY      601 ROEQSLLRHSVTNSQSGSPAPGRHDTLSKAGSDADGDSRSDSPLPHPFGKSDMFWYAR 660
DB      601 ROEQSLLRHSVTNSQSGSPAPGRHDTLSKAGSDADGDSRSDSPLPHPFGKSDMFWYAR 660
QY      661 EAAASAILGIDOKISHTLTDDELALFDVQKARAVRGLVEDNEDSSQSSFFPRDKYMSN 720
DB      661 EAAASAILGIDOKISHTLTDDELALFDVQKARAVRGLVEDNEDSSQSSFFPRDKYMSN 720
QY      721 GTINDPFLDTATITMPGTPRSSDDGDALFFGDGKSKODASNVNVEELRQOQAOWEBAKTA 780
DB      721 GTINDPFLDTATITMPGTPRSSDDGDALFFGDGKSKODASNVNVEELRQOQAOWEBAKTA 780
QY      781 KOEF 784
DB      781 KOEF 784

```

```

XX      KW      gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX      OS      Homo sapiens.
XX      PN      WO2004023973-A2.
XX      PD      25-MAR-2004.
XX      PF      12-SEP-2003; 2003WO-US028227.
XX      PR      12-SEP-2002; 2002US-0410259P.
XX      PR      12-SEP-2002; 2002US-0410260P.
XX      PA      (INCY-) INCYTE CORP.
XX      PI      Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI      Harshborne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,
PI      Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
PI      Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,
PI      Peralta CH, Anderson SB, Rioux P, Shen ED, Wu MC, Scuve LL,
PI      Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitec UA, Kilton ES,
PI      Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI      Patury S, Shi X, Suarez CJ;
XX      DR      WPI: 2004-329368/30.
XX      DR      N-PSDB; ACN42300.
XX      PT      New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX      PT      in diagnosing a condition, disease or disorder associated with human
XX      PT      molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX      PS      in gene mapping.
XX      PS      Claim 27; Page: 190pp; English.
XX      CC      The invention relates to novel diagnostic and therapeutic polynucleotides
XX      CC      selected from one of the 2722 sequences defined in the specification. A
XX      CC      polynucleotide of the invention may have a use in gene therapy. The human
XX      CC      diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
XX      CC      used to diagnose a particular condition, disease or disorder associated
XX      CC      with human molecules, e.g. cell proliferative disorders,
XX      CC      autoimmune/inflammatory disorder, developmental disorder, endocrine
XX      CC      disorder, neurological disorders, gastrointestinal disorders, or
XX      CC      infections caused by virus, bacteria, fungi or parasite. The dithp
XX      CC      molecules may also be used in genetic mapping, in identifying individuals
XX      CC      from minute biological samples, in detecting single nucleotide
XX      CC      polymorphisms, as molecular weight markers, and for somatic or germline
XX      CC      gene therapy. The present sequence represents a dithp protein of the
XX      CC      invention. Note: The sequence data for this patent is not represented in
XX      CC      the printed specification, but was obtained in electronic format directly
XX      CC      from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX      SQ      Sequence 1714 AA;
Query Match      41.8%; Score 1684.5; DB 8; Length 1714;
Best Local Similarity 46.5%; Pred. No. 6.4e-119;
Matches 358; Conservative 127; Mismatches 174; Indels 111; Gaps 16;

QY      4  GGNITVYVVRPPNAREIDRGACIYRMESGNOTITLPPGAEKARKSGKTTIDGPKAPA 63
DB      3  GASVYVAVVRPPNAREIDRGACIYRMESGNOTITLPPGAEKARKSGKTTIDGPKAPA 63
QY      64  PDRSYWSPDKNAP---NYARQEDLFQDLGVPLLDNAFKGNNNCIFAYGOTSGSKSYMMG 120
DB      52  FDIYSTWS--HTSPEDINAFSQQVYRDIGBEVLOHAFEGYVNCIFAYGOTGAGSYMMG 109
QY      121 YGK--EHGVIPRICODMERRINELQDKNLTCTVEVSYLEIYNERVRLDLPSTKGNLKV 178
DB      110  KOEKDQGGIIPQLGDLFSRINDTTND--NMGYSVSVSMETICEVRVRLDLPKGNLRLV 168
QY      179  REHPSGTPIYVEDLAKLVYRSFOEIEENLMDENGNKARTVAATNMNETSSKSHAVFTLTQK 238
DB      169  REHPLGTYVEDLSKLAVTSYNDIODLMDSGNKARTVAATNMNETSSKSHAVFTLTQK 228

```

RESULT 2
ABM63648 standard; protein; 1714 AA.
ABM63648;
18-NOV-2004 (first entry)
Human diagnostic and therapeutic pprotein SEQ ID NO:3897.

```
QY 239 WHDETMDTEKAKISLVLAGSERATSTGATGARKLKEGAINRSLTIGRVIALADM 298
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 229 RHDAETNITTEKYSKISLVLAGSERADSTGAKTRLKEGANINKSLTTIGKVISALAE 288
QY 299 SSG-----KOKNOQVYPRDSVLTWMLKDSLGNSTMTAMIAISPADINFEETLSTLYA 353
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 289 DSGNNKMKKKKKTDFIPYRDSVLTWMLRENLGNSTMTAMIAISPADINDETSTLYA 348
QY 354 DSAKRIRKHAHVNNEDPAPARMIRELKEELAQRLSKLSSGGGG-----GGAG----- 399
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 349 DRAKQIRCNVAVNNEDPNNKILRELKDEVTLRDLVLAQGLDITDNTVPGPKYVSLE 408
QY 400 -----GSGGPVEESYPPDTPLEKQIVSIQOPDATVKKMS-----KAEI 437
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 409 NNNLNKGCTVNEAPDPLSTVTNALVGM-SPSSSLASLSRAASVSLHERILFAPGSEEA 467
QY 438 VEOQNOSEKLYRDLNQTWEKLAETIEIKEREALAEELGISIEK--GVVGPYHSKEMPH 495
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 468 IERLKETEKTIAELINETWEKELRTEAIRMERELALAEKVAMRREDGTLGVSPKKT 527
QY 496 LVNLSDPDLAECIVYNIKPGQTRVGNVNDTQAEIRLNGSKILKEHCTFEN-----VDN 550
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 528 LVNLNEDPLMSECLLYIKDGITRVGREDERRQDIVLSGHFIKEHCVRSDSRGSGSEA 587
QY 551 VVTIVPNEKAAVWVNGVRIDKPTRLRSGYRIILGDPHIFRFNHPPEARARQEOSLLRHS 610
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 588 VVTLPECGADTVYNGKKTPEPILRSGNRIIMKSHVFFNHPQARQERER----- 640
QY 611 VTNSQLSGPAPGRHRTLSKAGSDADGSRSDSPLPFRFGKDSDFYARREAAAILGLD 670
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 641 -----TPCAETPAEPVDMAPAQRELLIEK-QGID 667
QY 671 QKISHLTDELDALFDVQKARAVRGVLEDNEDSDSSGSPVRDKMSN 720
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 668 MK--QEMEQRLQLELDQYRREDEATYLL-QQRLDESLEALQKQMS 714

RESULT 3
ABM83647
ID ABM83647 standard; protein: 1721 AA.
XX ABM83647;
AC ABM83647;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3896.
XX
KM gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartshorne TA, Suchorolski MT, Altue CM, Plets SJ, Elder LV;
PI Mooney BM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevany KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LT;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES;
PI Xu Y, Kwong W, Policky JU, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Fatury S, Shi X, Suarez CJ;
XX
MPI; 2004-329368/30.
```

```
DR N-PSDB; ACN42299.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27, Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
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CC from WIPD at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 1721 AA;
Query Match 41.8%; Score 1684.5; DB 8; Length 1721;
Best Local Similarity 46.5%; Pred. No. 6,5e-119;
Matches 358; Conservative 127; Mismatches 174; Indels 111; Gaps 16;
QY 4 GGNIVYVRRPNAEIDRGACIVRMENQIILPPPEAKKRSKGTINDGKAPA 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 GASVKVAVRVRPNSEKSRDSKCIITQMSGSTTVINPQPKET-----PSSFS 51
QY 64 FDRSYVSPDKNAP--NYARQEDLPQDLGVPLDNAFAKGNNCIFAYGQTSKSYSMG 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 52 FDSYVMS--HTSPEDINVASQKQVYRDIGEMLOHAFEGNVICIFAYGQTSKSYSTMG 109
QY 121 YGK-EHGVIPRIQDMFRINELQKDKLJTVEVSYLEIYNERVDDLNPSTKGLKV 178
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 KQEKDQGGIIPQCEBDFSRINDTND-NMYSVEVSYWEIYCEVRDLNPNKGNLRY 168
QY 179 REHPSTGPYVEDLAKLVASFOEINLMDGNKARVAAATNNGETSSRSAAVTLTLTK 228
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 169 REHPPLGYPVEDLSKLVASVINDIOPLMDSGNKARTVAATNNGETSSRSAAVENIIFTK 228
QY 239 WHDETMDTEKAKISLVLAGSERATSTGATGARKLKEGAINRSLTIGRVIALADM 298
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 229 RHDAETNITTEKYSKISLVLAGSERADSTGAKTRLKEGANINKSLTTIGKVISALAE 288
QY 299 SSG-----KOKNOQVYPRDSVLTWMLKDSLGNSTMTAMIAISPADINFEETLSTLYA 353
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 289 DSGNNKMKKKKKTDFIPYRDSVLTWMLRENLGNSTMTAMIAISPADINDETSTLYA 348
QY 354 DSAKRIRKHAHVNNEDPAPARMIRELKEELAQRLSKLSSGGGG-----GGAG----- 399
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 349 DRAKQIRCNVAVNNEDPNNKILRELKDEVTLRDLVLAQGLDITDNTVPGPKYVSLE 408
QY 400 -----GSGGPVEESYPPDTPLEKQIVSIQOPDATVKKMS-----KAEI 437
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 409 NNNLNKGCTVNEAPDPLSTVTNALVGM-SPSSSLASLSRAASVSLHERILFAPGSEEA 467
QY 438 VEOQNOSEKLYRDLNQTWEKLAETIEIKEREALAEELGISIEK--GVVGPYHSKEMPH 495
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 468 IERLKETEKTIAELINETWEKELRTEAIRMERELALAEKVAMRREDGTLGVSPKKT 527
QY 496 LVNLSDPDLAECIVYNIKPGQTRVGNVNDTQAEIRLNGSKILKEHCTFEN-----VDN 550
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 528 LVNLNEDPLMSECLLYIKDGITRVGREDERRQDIVLSGHFIKEHCVRSDSRGSGSEA 587
QY 551 VVTIVPNEKAAVWVNGVRIDKPTRLRSGYRIILGDPHIFRFNHPPEARARQEOSLLRHS 610
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Db 588 VVTLPECEGADTVYNGKVTBPSILRSGNRITIMGKSHVFRFNNPEQARQERER----- 640
Oy 611 VVNSQLGSGAPRGRHRTLSKAGSDADGDSRSDSPLEPHFGKOSDMFYAREASALIGD 670
Db 641 -----TPCAETPAEPVDMAFAQRELLER-OGID 667
Oy 671 OKISHLTDELDALFPDVOKARAVRGGLVEDNEDSDSSGSPFVRDKYMN 720
Db 668 MK--QEMGRLOLEBDQYRREBEATYLLF-QQRLDYSEKLEALQKOMS 714

RESULT 4
ABM83671

ID ABM83671 standard; protein; 1199 AA.

AC ABM83671;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic protease protein SEQ ID NO:3920.

KM gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.

OS Homo sapiens.

PN MO2004023973-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

(INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hachshorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerecht EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Klinton ES,
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patry S, Shi X, Suarez CJ;

DR WPI; 2004-329368/30.

DR N-PSDB; ACN42323.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

Claim 27; Page: 190DP; English.

The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorders, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The ditnp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germ-line
CC gene therapy. The present sequence represents a ditnp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

SQ Sequence 1199 AA;

Query Match 41.7%; Score 1679; DB 8; Length 1199;
Best Local Similarity 41.8%; Pred. No. 9,8e-119;
Matches 385; Conservative 139; Mismatches 232; Indels 164; Gaps 21;

Oy 4 GGNIVYVVRPPFNAREIDRGAKCIVRMEGNTLTTPPGAEKARKSKGTIMDGPFA 63
Db 3 GASVAVAVRPPFNAREIDRGAKCIVRMEGNTLTTPPGAEKARKSKGTIMDGPFA 51
Oy 64 PDRSYWSP-DKNAIPYARQEDLPQDLGVPLDANAFKGNVNCIFAYAGTSGSKSYSMGVG 122
Db 52 PDYSYWSHTSPEDPCFASQNRVYNDIGKEMLLHAEGVNCIFAYAGTSGSKSYSMGVG 111
Oy 123 KEH--GVTPRICODPFRINELQDKNLTCTVEVSYLEYIYNERVYDNLNPTSGNLKYRE 180
Db 112 EESONGIIPOLCEELFEKIND-NCEEMSYEVSYMYETICERVYDNLNPKKGNLRARE 170
Oy 181 HPSTGPVVEDLAKLVVRSFOEINEMDEGNKARTVAATNMNETSSRSHAVFTLTQKWH 240
Db 171 HPLIGPYVEDLSKLAVTSTYTDIADMDAGNKARTVAATNMNETSSRSHAVFTLTQKWH 230
Oy 241 DEETKMDTEKYAKISLVPLAGSERATSTGATGARLKEGAEINRSUSTIGRYIAALADN-- 298
Db 231 DNETNLSTEBKYSKISLVPLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEVDN 290
Oy 299 ---SSGKQKQQLVPRDSVLTWLLKDSLGGNSMTAMTAAISPADINFEETSLTRYADS 355
Db 291 CTSKSKKKKKKTDFIYRDSVLTWLLKDSLGGNSMTAMTAAISPADINFEETSLTRYADS 350
Oy 356 AKRIKNAHVNEDPNAFMIRELKEELAQRSKLSGSGGG-----GGAG----- 399
Db 351 AKQIKNAVINEDPNAKVLRELKEEVRTLKDLRAQGLDITIDPLIDYSGSGSKYLK 410
Oy 400 -----GSGPVEESYPPDPTLEKQ-----IVSTQPPATYKK 431
Db 411 DFQNNKRRYLLASENQRPHFSTASMGSLTSS-PSSCSLSQVGLTSTYSIQ-ERIMST 467
Oy 432 MSKAEIVLNQSEKLYVDLNOTWEKLAETEEIHKEREALEELGISIEK--GEVGPYH 489
Db 468 PGGEAIRELKESEKTIENLNETWEKLRKTEALRMEBALLAEAGVAIREDGGTLGVFS 527
Oy 490 SKEMPHLVNLSDDPLLAECGLVYNIKPGQTRVGNVNOTQAEIRLNGSKILKEHCTFENV- 548
Db 528 PKKTPHLVNLNEDPLMSECLLYYIKDGIYRGQDAERQDVIIVLSGAHIKEHCIFRSEB 587
Oy 549 ----DNVTIYVNEKAAVMNNGVRIDKPTRLRSGYRIILGDPHIFRHHPEEARER--- 601
Db 588 SNSGEVITVLEPCERSETTYNGKRVSPVQLRSGNRITIMGKSHVFRFNNPEQARERERT 647
Oy 602 -----QEOSLRLHSVTNSQ-----LGSAPRGRHRTLSKAGSDA 635
Db 648 PSAETPSPVDWTPAQRELLERKQIDMKQEMEKRLQEMELIYKKEKEADLLBEQRIDA 707
Oy 636 DGDSDSDS-----PDPHFR 649
Db 708 DSDSDSDSDKSCSESWKLITSLREKLPSPKLTQIVKKCGLPSSGKKREPIKMYQIPQR 767
Oy 650 --GKSDPFYARREASAILGLDQKISHLT-----DELALFPDVOKARAVRGGLVEDN 702
Db 768 RLSSKSKWVTISDLKIQVKEICYEVA-LNDFRRSRQIEALIVKMELCAMYGKQDPN 826
Oy 703 ESDSDSFPVARDKXNSGTIDNFSLPDPAITMPTGPRSD-----DGDALFFGDKSKXOD 757
Db 827 E-RDSWRAY-ARDVWDITGVGDEKEDVMAIGKSTVDVLDKMHDKLEDILQEVKKQNN 884
Oy 758 ASNVDEELRQQAQMEAL 777
Db 885 MKDEIKVILRNMLKMEKVL 904

RESULT 5
ABM83653

ID ABM83653 standard; protein; 1696 AA.
 XX ABM83653:
 XX
 XX 18-NOV-2004 (first entry)
 XX
 XX Human diagnostic and therapeutic pprotein SEQ ID NO:3902.
 XX
 XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
 XX Homo sapiens.
 OS
 PN WO2004023973-A2.
 XX
 XX 25-MAR-2004.
 PD
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 XX (INCY-) INCYTE CORP.
 PA
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
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 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu KC, Stuve LJ;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vicit UA, Kitson ES;
 PI Lu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX
 DR WPI: 2004-329368/30.
 DR N-PSDB; ACN42305.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 PS
 XX Claim 27, Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorder, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dthp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germ-line
 CC gene therapy. The present sequence represents a dthp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPD at www.wipo.int/pct/en/sequences/listing.htm
 CC
 XX
 SQ Sequence 1696 AA;
 Query Match 41.6%; Score 1674.5; DB 8; Length 1696;
 Best Local Similarity 46.4%; Pred. No. 3.7e-118;
 Matches 356; Conservative 128; Mismatches 175; Indels 109; Gaps 16;
 QY 4 GGNIKVVRVPPNASEIDRGAKCIVRMENQITLTPPGAEEKAKSGKTIINDGPKAFA 63
 DB 3 GAVKVAVRVPPNASEIDRGAKCIVRMENQITLTPPGAEEKAKSGKTIINDGPKAFA 63
 QY 64 FDSVYSFDPKAP--NYARQEDLPQDLGVPLLDNAFKYNNCIPAYGQSGSGKSYMMG 120
 DB 52 FDSVYS--HTSPEDINVASQKQVYRIGEMLOHAFEGYNVCIFAYGQSGAKSYMMG 109

QY 121 YGR--EHGVIPRICODMFRINELQDKQNLCTVEVSYLEINERYVDLNPSTKGLKY 178
 DB 110 KQKDDGGIIPQCEBDFSKINDTND--NMSYVEVSYMEIYGERRDLLNPKNGKLRY 168
 QY 179 REHPSTGPVYEDIKLVNSFOEINELMDGKARFVAATNMNETSSRSNAVFTLTQK 238
 DB 169 REHPLLGPVYEDLSKLVNSYNDIODLMDSGKARFVAATNMNETSSRSNAVFNIFTQK 228
 QY 239 WHDEETKMDPEKAKISLVNLAGSERATSGAAGALKKEAEINRSLTGRITAAADM 298
 DB 229 RHDLENTITTEKYSKISLVNLAGSERADSTGAGTRLKEGANINKSLTTLGKVISALAE 288
 QY 299 ---SSGKOKKQVLVPRDSVLTWLLKDSLGSGNMTAMIAISPADINFEETLTSLRAD 355
 DB 289 XPPONKKKKKTDFIPRDSVLTWLLRBNLGNSRTAMVAALSPADINDTLTLRYADR 348
 QY 356 AKRIKHAHVNEDPNAMRIELKEELAQRLKQSSGGG-----GGAG----- 399
 DB 349 AKQIRGNAVINEDPNKLTRELKDEVTYRLDLLYAQGLGIDTDTNTVPGGPKYVSDLENN 408
 QY 400 --GSGRPVESYPPDPLEKQIVSIQPDATVKKM-----KAEIVE 439
 DB 409 NLRGGTVNEAPDPLSTVTNALVGM--SPSSLSALSSRAVSLSLHERILFAPGSEPAIE 467
 QY 440 QLNQSEKLYRDNLQGTWEKLAKEEIHKEEALBEIGISIEK--GFVGYHSEKMPHLV 497
 DB 468 RLKETEKIIELEWETBEKLRRTETALRMERREALAEKVAMRDGGTLGVFSKPKPHLV 527
 QY 498 NLSDDPLAECLVYNIKPGQTRGVANNODTOAERLNGSKILNEHGFEN-----VDNVV 552
 DB 528 NINEDPLMSECLLYIKDGITRVGRDGERRODIVLSGHPIKEHCYFRSDSGSBAYV 587
 QY 553 TIVPNEKAVMNVGVAIDKPTRLRSGRTIILGDFHFRFNHPEAEARQESLLNHSVT 612
 DB 588 TLEPCGADTYNGKKTVEPSILRSNGRIIMGKSHVFRNHPQAOEER----- 638
 QY 613 NSQLGSPAPGRHRTLSKAGSDADGDSRDSPLPHFRGKDSDFVYARREASAILGDDOK 672
 DB 639 -----TPCAETPAEVDVMAFQRELEER--QGITDMK 667
 QY 673 ISHLTDELDALEFDVQKARAVRGLVEDNEDSDQSFPVRDKYMSN 720
 DB 668 --QEMQRLOLELDQYRRRREAEATYLE--QQRIDYVSKLEALQKQMS 712
 RESULT 6
 ID ABM83649 standard; protein; 1709 AA.
 XX
 XX ABM83649:
 XX
 XX 18-NOV-2004 (first entry)
 XX
 XX Human diagnostic and therapeutic pprotein SEQ ID NO:3898.
 XX
 XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
 XX Homo sapiens.
 OS
 PN WO2004023973-A2.
 XX
 XX 25-MAR-2004.
 PD
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 XX (INCY-) INCYTE CORP.
 PA
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
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 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PT Stevens KA, Blanchard JB, Panzer SR, Wang X, Au AP, Geregin EH;
 PI Petralia CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;
 PI Lagace RE, Spiro PA, Stewart AJ, Wingoore J, Velt UA, Kitron ES;
 PI Xu Y, Kwong M, Pollicky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX
 DR WPI: 2004-329368/30.
 DR N-PSDB; ACN42301.
 DR XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
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 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
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 XX
 PS
 XX
 Claim 27, Page; 190pp, English.
 XX
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 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC polynucleotide of the invention may have a use in gene therapy. The human
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 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorders, developmental disorders, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The ditnp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a ditnp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 CC
 XX
 XX
 Sequence 1709 AA;
 QQ

Query Match	41.6%	Score 1674.5	DB 8	Length 1709
Best Local Similarity	46.4%	Pred. No. 3.7e-118		
Matches 356	Conservative 128	Mismatches 175	Indels 109	Gaps 16

[illegible]

Db	466	RLKETEKIIAELNETWEKLRRTFAIRMERREALLAEMVAREDDGGTILGVFSPKCTPHLV	527
Qy	498	NLSDDPLLAECVLVYIKKPGCTVGVNVNODTQAEIRLNGSKTLKHKCFPEN-----VDNVV	5523
Db	528	NLMEDELMECCLLYIKDKGITVGVDEDERRODIVLSHPIFKESHCFVRSRSGSAVV	587
Qy	553	TIYPNKAALVWNGVVIDKPTRLRSQYRIILGDPIIFPFNHPPEARARQEQSLRHSTV	612
Db	588	TLSPCEADLTYYNGKKVVEPSTLRSGNRIIMGKSHVFNFHPEQARQERK-----	638
Qy	613	NSQLGSPAPGRHDIRTLSSKASGDADSDRSRSPLPPIFRCKSDMFEVYARREASAILGDOK	672
Db	639	-----TPCAETPAEPVDMFAQRELLEK-QGIDMK	667
Qy	673	ISHLTDELDALEFDYQKARAVRGLVEDNEDSDSQSFPPVDRKXMSN	720
Db	668	--QEMEQRLQLEDDQYRREREAEATYLE-QORLDYESKLEALQKQMS	712
RESULT 7			
XX	ABM83646	standard; protein; 1722 AA.	
XX	ABM83646:		
XX	18-NOV-2004	(first entry)	
XX	Human diagnostic and therapeutic pprotein SEQ ID NO:3895.		
XX	gene therapy; human diagnostic and therapeutic polynucleotide; dtlcp.		
XX	Homo sapiens.		
XX	MO2004023973-A2.		
XX	25-MAR-2004.		
XX	12-SEP-2003; 2003WO-US028227.		
XX	12-SEP-2002; 2002US-0410259P.		
XX	12-SEP-2002; 2002US-0410260P.		
XX	(INCY-) INCYTE CORP.		
XX	Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F, Hartshorne TA, Suchorolski MT, Altus CM, Plets SD, Elder LV; Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP; Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH; Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL; Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitron ES; Xu Y, Kong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D; Patury S, Shi X, Suarez CJ;		
XX	WPI: 2004-329368/30.		
XX	N-PSDB; ACN42298.		
XX	New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.		
XX	Claim 27; Page; 190pp; English.		
XX	The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dtlcp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dtlcp molecules may also be used in genetic mapping, in identifying individuals		

CC from mitre biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a d1tp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/1listing.htm
CC

SQ Sequence 1722 AA;

Query Match	41.6%	Score 1674.5	DB 8	Length 1722
Best Local Similarity	46.4%	Pred. No. 3.8e-118		
Matches 356	Conservative 128	Mismatches 175	Indels 109	Gaps 15

```

QY 4 GGNIKVAVVPPFNAAEIRGAKCIVIRMEGNQNTILTPPGAEEKARSAKGTIMDGPAFA 63
D 3 GAVKAVAVVPPFNSEMRSDSKCIIQMSGSTTTIVNPKQKET-----PKSFS 51
QY 64 FDRSYWSPDKNAP--NVAQEDLFODLGVPLLDNAFGKYNNCI PAYQGTSGSKSYSMG 120
D 52 FDSYSYS--HTSPEDINVAQKQVRYDICEBMLQHAPEGVNVCI PAYQGTGAGKSYTMG 109
QY 121 YGR--BHGVIIPRIQDMFRINELQDKXKLTVEVSLIETIYNERVADLPNPSKGNLKY 178
D 110 KQEKDQGGIIPOLCEBDFSRINDTND--NMSYSVEVSYMEIYCEBRYVDLPNPKKGLRV 168
QY 179 REHPTGTPVEDLAKLIVYRSFOEINLMDCEKARTVAATMMNETSSRSHAVFTLLTQK 238
D 169 REHPLLGPVEDLSKLAATSYNDIQDLMDGSKARTVAATMMNETSSRSHAVFTITQK 228
QY 239 WHDEETKMDTEKVAKISIVDLAGSERATSGATGARLKEGAINRSISTLGRVIALADM 298
D 229 RHAETNITTEKYSKISIVDLAGSRBADSTGAKGRLEKGANINKSLITLIGKVISALAEM 288
QY 299 ---SSGQKKKNQVLVPRDSVLTWLLKDSIGKNSMTAMIAISPADINFEETLSTLRVADS 355
D 289 XRPQNKKKKKKTDFIPIRDSVLTWLLRENLGKNSRTAMVAALSPADINVEDTLSTLRVADR 348
QY 356 AKRIKHAIVVNDPNARMTRELKEEADLRSLKLSGSGGCG-----CGAG----- 399
D 349 AKQIRCNAAVINDPNNKLRELKEDVTRLRDLVLAQGLDITDNTVPGGPKVYSDLENN 408
QY 400 --GSGGPVSESYPPDTLEKQIVSIIQOPDATVYKMS-----KAEIYE 439
D 409 NUNRGTTVEADPELSTYTNMALVGM--SSSSLSALSSAASVSSLHERILFAPROSEATE 467
QY 440 QLNQSEKLYRDINQWEEKLAETBEEIHKEREALAEIGISIEK--GFGVGYHSKEMPHLY 497
D 468 PLKETEKIIAEINETWEEKLRTEAIRMERREALLAEMGVAMREDDGTLGVFSPKPTPHLY 527
QY 498 NLSDDPLLAECVLVNIKQGTQVGVGNVNDQTAERPLNGSKILKHCFTFEN-----VDNVY 552
D 528 NINEDPLMSECLLYYIKGITVVGEDDERRODIVLSGHFIKEBHCYFRDSRSGSEAVY 587
QY 553 TIIVPNKAAVWNGVRIIDKPTRLRSGRYIIGLDFIIFPNHPEBAREROQSILHRSVY 612
D 588 TLEPCGADTYNGKKTVEPSILRSGNRIIMGKSHVRFNHPBAROERER----- 638
QY 613 NSQLGSPADGRDRTLKSGADSDSRSDPLPHFRKSDSWFVARREASAAILGLDOK 672
D 639 -----TPCAETPAEPVDVMAFAQRELLER-QGIDMK 667
QY 673 ISHLTDDDELALFDVOQAKARAVRGLVADNEDSDSGSFPFRDKRYMKN 720
D 668 --QEMEQRLQBLEDDYRRREBETATYLB-QQRLVYESLUALQOMDS 712

```

RESULT 8
ABM83650
ID ABM83650 standard; protein; 1708 AA.

DT 18-NOV-2004 (first entry)

XX	Human diagnostic and therapeutic pprtein SEQ ID NO:3899.
DE	

gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

OS Homo sapiens.

PN WO2004023973-A2.

PD 25-MAR-2004

PF 12-SEP-2003; 2003WO-US028227

PR 12-SEP-2002; 2002US-0410259P

XX XX

PA (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gi

XXXXXXXXXXXX

DR N-PSDB; ACN42302.

PT New diagnostic and therapeutic polynucleotides and polypeptides,

PT molecules, e.g. autoimmune or inflammatory disorders, in gene the

[illegible]

Db	169	REHPPLGPIVEDUSKLAIVTSYNDIDQDLMGSGKAKATVAATNNNETSSSHAVFNITFOK	228
Qy	239	WHEETKMDTEKAKIAKISLVLDAGSERATSTGATGARLKEGAETNRSSTLGRVIALADAM	298
Db	229	RHDAENITITTEKXSKISLVLDAGSERADSTGAKGRRLKEGANINNSLTTLTKVIALAEM	288
Qy	299	SGG-----KOKKQQLVPRYDSVLTWLLKQSLGNSMTAMIAAISPADINFEETSLTRYA	355
Db	289	DSQPNKKKKKKKTDFIPYRDSVLTWLLRENLGNSRTAMVAALSPADINDETSLTRYA	348
Qy	354	DSAKRIKNHVVNVEDNNAIMIRELKEELQSLQSSGGGGGGGSGSGPVESEYPTD	413
Db	349	DRAKQIRCNVAVNVEDNNKILRELQDEVRLDLV-----AQGGIDITDTNTPGCG	400
Qy	414	PLEKQIVSIQOPDATYKKMS-----KAEIVEQLNQSERYLDLNOQTW	455
Db	401	PXLTNLVGMSPESSLSLALSSRAASVSLHERILFPAPGEKALIELKXTEKILNELNBTW	466
Qy	456	EEVKLAKTEIEHKEREALBELGISIEK--GVGYPHSKEMPHLVNLSDDLPLAECLVYNI	513
Db	461	EEKLRRTREALRMERREALLEMGVAMREDGTLGVFSPKTPHLVNLNEDPLMSECLLYYI	520
Qy	514	KPGQTVGNVNOQTOAEIRLNGSKILKECTEN-----VDNVVTIYVNEKGAVMNNGVR	566
Db	521	KDQITRVGRDGERRODIVLSCGFIEKHCFRSDRGSEAVVTLFPCESADITYVNGKK	580
Qy	569	IDKPTRLSGYRIILGDFHIFRPNHEEARAEQOSLIRHSVTNSQLDSPAQRHRTL	628
Db	581	VTEPSILRSGNRLTIKMSKSHVFRPNHEQAKQERER-----	615
Qy	629	SKAGSDADGDSRSDSPLPHFRGKDSDFYARREASAILGLDQKISHLTDELDALFDV	686
Db	616	-----TPCAETPAEPVDVMAFAQRELLK--QGIDMK--QEMEQLQLEBDQY	658
Qy	689	QKARAVRGLVEDNEDSDQSSSPVPRDKYMSN	720
Db	659	RREREATYLL--QORLDYESKLEALQKQMS	689

RESULT 9

ABM83651

ID ABM83651 standard; protein; 1699 AA.

XX ABM83651;

XX

AC

XX

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pproetin SEQ ID NO:390.

XX

KW gene therapy; human diagnostic and therapeutic polynucleotide; dihp.

XX

OS Homo sapiens.

XX

PN WO2004023973-A2.

XX

PD 25-MAR-2004.

XX

PF 12-SEP-2003; 2003WO-US028227.

XX

PR 12-SEP-2002; 2002US-0410259P.

XX

PR 12-SEP-2002; 2002US-0410260P.

XX

PA (INCY-) INCYTE CORP.

XX

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,

PI Harthshorne TA, Suchorolski MT, Altue CM, Plets SJ, Elder LV,

PI Mooney EM, Deleagane AM, Panssar IS, Banville SC, Reddy TP,

PI Stevens KA, Blanchard JL, Panser SR, Wang X, Au AP, Gerstin EH,

PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LT,

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitron ES,

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,

PI Patury S, Shi X, Suarez CJ;

XX	WPI: 2004-329368/30.
DR	N-PSDB; ACN42303.
XX	New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT	in diagnosing a condition, disease or disorder associated with human
PT	molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT	in gene mapping.
XX	
PS	Claim 27; Page; 190pp; English.
CC	The invention relates to novel diagnostic and therapeutic polynucleotides
CC	selected from one of the 2122 sequences defined in the specification. A
CC	polynucleotide of the invention may have a use in gene therapy. The human
CC	diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC	used to diagnose a particular condition, disease or disorder associated
CC	with human molecules, e.g. cell proliferative disorders,
CC	autoimmune/inflammatory disorder, developmental disorder, endocrine
CC	disorder, neurological disorders, gastrointestinal disorders, or
CC	infections caused by virus, bacteria, fungi or parasite. The dithp
CC	molecules may also be used in genetic mapping, in identifying individuals
CC	from minute biological samples, in detecting single nucleotide
CC	polymorphisms, as molecular weight markers, and for somatic or germ-line
CC	gene therapy. The present sequence represents a dithp protein of the
CC	invention. Note: The sequence data for this patent is not represented in
CC	the printed specification, but was obtained in electronic format directly
CC	from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX	
SQ	Sequence 1699 AA:
Query Match	41.4%; Score 1669.5; DB 8; Length 1699;
Best Local Similarity	46.8%; Pred. No. 8.9e-118;
Matches 352;	Conservative 125; Mismatches 166; Indels 109; Gaps 15
OY	4 GGNKVVVVRVPFNAAREIDRGAKCIVRWEGNOTILTPPGAEBEKKRKSCKTIMGPKAPFA 63
Db	3 GASVKVAARVAFPNRSREMSRDKSCITIQNGSGTTIVNEKPKEP-----PKFS 51
OY	64 FDRSYWSFDKNAP---NYAROEDLFODLGVLLDPAFGYNNCIFYAGOTGSGSKSYMWG 120
Db	52 FDYSYWS--HNSPEDINVASQKYVRDGEMLQAFGYNVCIFYAGOTGAGKSYTMWG 109
OY	121 YGR--EHGVIPRICODMFRINELOKDNULTCTVEVSYLEIYNERKVDRLNPSTGNLKV 178
Db	110 KQEKDOQGIIPLQCEDFLSFINDTND--NMSYSEVSMEIYEICERVDRLNPKNKGNLRV 168
OY	179 REHSSTGYGVDELKLTVRSFOELENLMDECNKARTVAATMMNERSSHAVFTLTLOK 238
Db	169 REHPVLGGYVDELKSLAATSVINDIODLSDSNKARTVAATMMNERSSSHAVFNIIIFOK 228
OY	239 WHDEETKMDTEKVAKISLVLDAGESERAVSTGATGARLEKGAINEKSLSTLRGVIALADM 298
Db	229 RHDAETNITEKESKISLVLDAGEBRADSTAKGRLEKANIKSLTLTKKVISALAEW 286
OY	299 SSG-----KQKNOLVPRDSVLTWLKDSLIGNSMTAMIAISPADINFEEETSLTRYA 353
Db	289 DSGPNKKKKKKCTDFIPYRDSVLTWLIRENLGNSRTAMVALSPADINYETISTLRYA 348
OY	354 DSARKIRKHANVMNDDPNARMRELKELBAOLAKSLTGSSGGCGGAGSGGCPVEBESPDP 413
Db	349 DRAQOIRRNAVINBDPNKKLRELKDEVTRLRLDLVLAOGIG-----DIT 392
OY	414 PLEKOIVSIOPDPAIVFKMS-----KAIEIVPOLNSEKLYRDLOTW 455
Db	393 DMTAALVGM--SPSSLALSRRASVSLSHRILPAPSEBEAIRLKTETKIIALNETW 451
OY	456 EEKLAKTEELHKEREAALEELGISIEK--GFVGPHYSXEMPHLVNLSDDLAECLVNI 513
Db	452 EEXLRRTETAIEMEREDALLAEKGVAMREDGGTLGVFSPKKTDLVLVNLEDPLMSSECLYVI 511
OY	514 KPQGTGRGANVNOQTQABIRLNGSKILKEHCFFEN----VNVVTIVNEKRAAVNVANGVR 568
Db	512 KDGTTRVGREGBERODIVLSGHFIKEHHCVFRSDSRGSAVVTLPECEGADVTVNGKK 571

Db 468 IERLKESEKIIAEINLTWESEKLRKTEAIRMERALLAEMGVAIREDDGTLGVFSPKPTPH 527
Qy 496 LVNLSDDDLAECLVYNIKPGQTRVGNVNDTOAEIFLNSKILKEHCTENV-----DN 550
Db 528 LVNLNEDPLWSECLLYIKDGIKTRVGADABRRDQIVLSGAHKEEHCFRSEKSNSEV 587
Qy 551 VVTIVPEKAAMVWNGVRIDKPTLRSGYRIILGDFIIFRNHPEEAROEQSLRH 610
Db 588 IVTLPEPERSELYNGKRVGQPVQLRSGNRIIMKGNHVFRRNPEQARERK----- 640
Qy 611 VTNSQLSPAPGRHRTLSKAGSDADGSDSPFLPHFRKSDWFIYARREASAILGLD 670
Db 641 -----TPSAETPSEPVDWTFPAQRELLLEK-OGID 667
Qy 671 QK-----ISHLTDELDALFDD-----VOKARAIVRGLVEDNEDSDS 707
Db 668 MKQEMERKLOEMELLYKKEKEADLLLEQQLDYESKLQALQKQVETRSILAETTEEBE 727
Qy 708 QSSFP 712
Db 728 EEEVP 732

RESULT 12
AAE35317
ID AAE35317 standard; protein; 1770 AA.

AC AAE35317;
XX
DT 17-JUN-2003 (first entry)

DE Mouse KIF1Bbeta protein.

KIF1B protein; gene therapy; molecular motor protein; kinesin; mouse;
KIF1Bbeta gene-associated disease; Charcot-Marie-Tooth disease type 2A;
muscular; transgenic.

OS Mus musculus.

PN MO200297079-A2.

XX 05-DEC-2002.

PF 29-MAY-2002; 2002MO-JP005226.

PR 29-MAY-2001; 2001US-0293513P.

XX (UYTY) UNIV TOKYO.

PI Hirokawa N, Hayaehi Y;

XX WPI, 2003-167270/16.

DR N-PSDB; AAD53964.

XX

PT New KIF1B polypeptide having motor activity that transports synaptic

PS vesicle precursor. is useful for developing therapeutic or preventive

XX agent for kif1b gene-associated diseases e.g. Charcot-Marie-Tooth

XX disease type 2A.

XX

XX Claim 1; Page 72-78; 44p; English.

CC The invention relates to KIF1B protein which belongs to kinesin
CC superfamily of molecular motor proteins (KIFs). KIF1B is useful for
CC screening for a compound binding to it. Composition comprising the
CC selected compound is useful for treating, alleviating, or preventing a
CC KIF1B gene-associated disease, in particular Charcot-Marie-Tooth
CC disease type 2A. Transgenic non-human vertebrate, are useful for
CC screening for a candidate compound for treating, alleviating, or
CC preventing a KIF1B gene-associated disease. KIF1B DNA is useful for
CC gene therapy and for recombinant production of polypeptides. KIF1B
CC antibody is useful for affinity purification of KIF1B and for detecting
CC expression of KIF1B gene at the protein level. The present sequence
CC is mouse KIF1Bbeta protein

XX
SQ Sequence 1770 AA;

Query Match 41.4%; Score 1666.5; DB 6; Length 1770;
Best Local Similarity 47.3%; Pred. No. 1,6e-117;
Matches 353; Conservative 125; Mismatches 174; Indels 95; Gaps 15;

Qy 4 GGNIKVVVRPRPNNAEIDRGACIYRMENQIILPPPAERKAKSKGTINDGPAFA 63
Db 3 GASVKAARVRPPNSRETSKESKCIIOQGNSTSIINPKPK-----APKSFS 51
Qy 64 FDRSYMSF-DKAPNPAROEEDLPQDLGVPLDPAFGYNNICPAYCOTSGSKSYMWGYG 122
Db 52 FDYSYMSHSPEDPCASQNRVYNDIGKMLHAFEGYVNCIFAYCOTGSKSYTMGKQ 111
Qy 123 KEH-GVIRICODMFRRIEOLKXNLCTYEVSYLEYNEKRVLDLNPSTGNLKVRE 180
Db 112 EESQAGIIPQLCELEPEKIND-NCNEMSYSEVSWEIYCERVRDILNPKGNLRVRE 170
Qy 181 HPSTGPIVEDLAKLVYRSFOEINLMDENKATVAATMNETSSRSNAVFTLTQKH 240
Db 171 HPLGPIVEDLSKLAATVSTYDIALMDAGNKATVAATMNETSSRSNAVFTLTQKH 230
Qy 241 DEETKMDTEKVAKISLVDLAGESEATSGATGARLKEGAEINRSLSLIGRVIAALDMSS 300
Db 231 DEPTNLSTKVKSKISLVDLAGESEATSGATGARLKEGAEINRSLSLIGRVIAALDMSS 230
Qy 301 GKQKQNLVPRYDVLTVLLKDSLGGNSMTAMIAISPADINEETLSTLYADSAKRIK 360
Db 291 -KKKTDPIPRYDVLTVLLRENLGGNSRTAMVAPALSPADINDETLSTLYADRAKQIK 349
Qy 361 NHAIVNEDPNAKIRIRLKEELAQLRKLSOSSGGGSGAGSGGPVESEYPPDPLEKQ-- 418
Db 350 CNAVINEDPNAKIRIRLKEELAQLRKLSOSSGGGSGAGSGGPVESEYPPDPLEKQ-- 407
Qy 419 ---IVSIQPDATVKKMSKAEIYEQUNOSEKLYRDINQWEEKLAKTEIRHKEEALAE 475
Db 408 LITSVTSIQ--ERIMSTPGGEAEIRLKESEKIIAEINLTWESEKLRKTEAIRMERALLAE 465
Qy 476 LGISIEK--GVGPGYHSMKEMPHLVNLSDDLAECLVYNIKPGQTRVGNVNDTOAEIRL 533
Db 466 MGVAIREDDGTLGVFSPKPTPHLVNLEDBPLWSECLLYIKDGIKTRVGADABRRDQIVL 525
Qy 534 NSGKILKEHCTENV-----DNVVTIVPEKAAMVWNGVRIDKPTLRSGYRIILGDFI 588
Db 526 SGAKIIEEHCLFRSEKSNSEVIVTLPEPERSELYNGKRVGQPVQLRSGNRIIMKGNH 585
Qy 589 FRNHPPEARAEAROEQSLRHSTVNSQLGSPAPGRHRTLSKAGSDADGSDSPFLPHF 648
Db 586 FRNHPPEARAEAROEQSLRHSTVNSQLGSPAPGRHRTLSKAGSDADGSDSPFLPHF 606
Qy 649 RGDSDWFIYARREASAILGLDQK-----ISHLTDELDAL-----FDDVOKA 691
Db 607 PSEPVDWTFPAQRELLLEK-OGIDMKQEMERKLOEMELLYKKEKEADLLLEQQLDYESTL 665
Qy 692 RAVRGL-----VEENEDSDQSFP 712
Db 666 QALQKQVETRSILAETTEEBEEVEVP 692

RESULT 13

AB807867
ID AB807867 standard; protein; 1823 AA.

XX AB807867;
XX

DT 03-JUL-2002 (first entry)

DE Human kinesin-associated protein having motor domain.

XX Human; kinesin-associated protein; motor domain; cytoskeletal; KIF1B-beta;
KW neuroblastoma.

XX

CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification

XX Sequence 893 AA;

Query Match 41.2%; Score 1660.5; DB 4; Length 893;
 Best Local Similarity 46.5%; Pred. No. 1.6e-117;
 Matches 350; Conservative 126; Mismatches 167; Indels 109; Gaps 15;

QY 4 GGNIKYVVRPFPNAREIDRGAKCIVRMEGNOTILTPPBAEKARKSGKTINDGPAPA 63
 DB 3 GASVKAARVRPFPNSRMSRDSKCIIOGSGSTTTIVNPKPKET-----PKSFS 51
 QY 64 FDRSYWSPDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGOTGSGKSYSMWG 120
 DB 52 FDSYSYA--HTSPEDINVASQKQVYRDIGBEMIOHAFEGNVICIFAYGOGAKSITMKG 109
 QY 121 YGK-EHGVIPRICQMFRRINELQDKMLTCTVEVSYLEIYNERVADLLNPSTKGLKY 178
 DB 110 KKKQDQGGIIPOLCEBDFSRINDTND-NMSYSEVSMEIYCEYERVDLLNPKKGLRY 168
 QY 179 REHPSRGVYEDLAKLVNRSFOEINLMDGNKARTYAAANNMETSRSRAVTLTLTK 238
 DB 169 REHPLGPPYVEDSKIAVTSYNDIQDLMDSGNKARTYAAANNMETSRSRAVFNIIFTOK 228
 QY 239 WHDEETKMDTEAKISLVLDLASERATSGATGARLKEGAEINRSISTGRVIALADM 298
 DB 229 RHAENITTEKSKISLVLDLASERADSTGAKTRKEANINKSLITLIGKVISALAE 288
 QY 299 SSG-----KOKKNQLVPRDSVLTWLLKDSLGNSMTAMIAISPADINEETLSTLRYA 353
 DB 289 DSGPNKKKKKKTKDFIPYRDSVLTWLLRENLGNSRTAMVAALSPADINDETSLTRYA 348
 QY 354 DSAKIRKNAVVNEDNARMIRLEKEELAQTRKLGSSGGGGGAGSGGSPVEESTPPT 413
 DB 349 DRKQIRCAVAVNEDPNKKLIRELKQEVRLRLDLVLAQGLG-----DIT 392
 QY 414 PLEKQIVSIQOPATVYKNS-----KAEIYEOJNOSEKLYRDINQW 455
 DB 393 DMYNALVGM-SPSSSIALSSRAASVSLHERLLFAPGSEAEIRLEKETIKTIAENETW 451
 QY 456 EEKLAETEEIHKERALEELGISIEK--GFVGRYHSEKMPHLVNLSDPLLAELVYNI 513
 DB 452 EEKLRTEAIRMERRELLAEWGAAMKEDGTLGVFSPKTPHLVNLNEDPIMSECLLYI 511
 QY 514 KPGQTVANNNOTQAEIRLNGSKILKEHTFEN-----VDNVYTVIENKAAVMMNGVR 568
 DB 512 KQGITVGRDEGRRDDIVLSGHFIRKEEHVCFVSDRSGSEAVVTLEPGCATYVNGKK 571
 QY 569 IDKPTRLSGQYRIILGDFHIFRNHPPEBARERQESLLRHSHTNQLQSPAPGRIDRTLI 628
 DB 572 VTRPSILRSGNRIIMKSHVFRFTHPQAKOERER----- 606
 QY 629 SKAGSDADSDSRSDPLPHFRGSDMFWAARREASAILGLDOKISHTLTDDELALFDV 688
 DB 607 -----TCAETPAEPVDWMAFQORELLEK--QGIDMK--QEMEQRLQELDEDY 649
 QY 689 OKARAIVRGLVEDNEDSDOSSFPVADKYMSN 720
 DB 650 RRREREATYLL--QORLDYESKLEALQKOWDS 680

RESULT 15

ID AAM38652 standard; protein; 1697 AA.

AC AAM38652;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pproetin SEQ ID NO:3901.

XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

XX Homo sapiens.

PN WO2004023973-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

PA (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,

PI Hartshorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Karton ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patry S, Shi X, Suarez CO;

XX MPI; 2004-329368/30.

DR N-PSDB; ACN42304.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful

PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

PS in gene mapping.

PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides

CC selected from one of the 272 sequences defined in the specification. A

CC polynucleotide of the invention may have a use in gene therapy. The human

CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be

CC used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorder, endocrine

CC autoimmune/inflammatory disorder, developmental disorder, endocrine

CC disorder, neurological disorders, gastrointestinal disorders, or

CC infections caused by virus, bacteria, fungi or parasites. The dthp

CC molecules may also be used in genetic mapping, in identifying individuals

CC from minute biological samples; in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline

CC gene therapy. The present sequence represents a dthp protein of the

CC invention. Note: The sequence data for this patent is not represented in

CC the printed specification, but was obtained in electronic format directly

CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 1697 AA;

Query Match 41.2%; Score 1659.5; DB 8; Length 1697;
 Best Local Similarity 46.7%; Pred. No. 5.2e-117;
 Matches 350; Conservative 126; Mismatches 167; Indels 107; Gaps 15;

QY 4 GGNIKYVVRPFPNAREIDRGAKCIVRMEGNOTILTPPBAEKARKSGKTINDGPAPA 63
 DB 3 GASVKAARVRPFPNSRMSRDSKCIIOGSGSTTTIVNPKPKET-----PKSFS 51
 QY 64 FDRSYWSPDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGOTGSGKSYSMWG 120

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Db 52 FDYSYMS--HTSPEDINVASQKQVVRDISEBMLQHAFEBGYNCIFPAYGQTGAKSKSYTMWG 109
Qy 121 YGK--EHGVIPRIQDMFERRINELQDKXLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
Db 110 KOEKQOQGIIPOLCEDLFGRINDTND-NMSYSVEVSYMEIYCERVYRDLNPNKGNLKV 168
Qy 179 RHPSTGPRVEDLAVLVNRSFOEIEMLMBEGKARTVAATNMNETSSRSHAVFTLLTQK 238
Db 169 RHPPLGPRVEDLSKLAVTSYNDIODLMSGNKARTVAATNMNETSSRSHAVFNITQK 228
Qy 239 WHDEETKMDTEKYAKISLVDLGSEKATSTGATGALKEGAEINRSLSLGRVIALADM 298
Db 229 RHDATNITTEKYSKISLVDLGSEKADSTGAKGTLKEGANINKSLTLGKVISALAE 288
Qy 299 ---SSGKQKQNLVPRDSVLTWMLKDSLGSNSMTAIAISPADINFEETLSTLRVADS 355
Db 289 XPPQNKKKKTDPIPRDSVLTWMLRENLGNSRTAMVAAISPADINDETSLTLRYADR 348
Qy 356 AKRIKNHVVNEDPNARMIRELKEELAKLSKLGSSGGGGAGSGGSPVEESYPPDPL 415
Db 349 AKQIRCNNAVINEDPNKLIRELKDEVTRLRLDLVYAGLG-----DITDM 392
Qy 416 EKQIVSIQOPDATVVKMS-----KAEIVQLNQSSEKLYRDLNQTWEE 457
Db 393 TNALVGM-SPSSSLSSLSRAASVSSLHRIILFAPGSEAEIERLKEKIIAELNETWEE 451
Qy 458 KLAETBEIHKERPALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECLYYNIKP 515
Db 452 KLRTETAIEMERREALAEMGVAMREDCGTLGVSPKTPHLVNLNEDPLMSECLLYYID 511
Qy 516 GQTRVGNVNODQAEIRLNGSKILKEHCPEFEN----VNVVTIVPNEKAAVWNGVRID 570
Db 512 GTRVGRREDGERODIVLSGHFIKEHCVPFRSDSRGSEAVVTLEPCBAGDTYVNGKKVT 571
Qy 571 KPTRLSGGRYIILGDFHIFRFNHPBEAPAROEOSILRHSVTNSQLGSPAPGRHRTLSK 630
Db 572 EPSILRSNGRIIMGKSHVFRFNHPBQARQERER----- 604
Qy 631 AGSDADGDSRSDSPLPHFRGKDSDFYARREASAILGLDQKISHLTDELDALEFDDVOK 690
Db 605 -----TPCAETPAPFPVDMFAQRELELEK-QGIDMK--QEMEQRLOLELEDQYRR 649
Qy 691 ARAVRGLVEDNEDSDSSSFVRDKYMN 720
Db 650 EREBATYLLLE-QORLDYESKLEALQKQKMS 678
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Search completed: September 1, 2006, 14:27:10
Job time : 194.583 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 1, 2006, 14:22:42 ; Search time 263.166 Seconds
(without alignments)
2755.725 Million cell updates/sec

Title: US-09-235-416-1
Perfect score: 4030
Sequence: 1 MSGGGNIKVVVRVPRNARE.....ELRQQAQMEALKTAKQER 784

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3966	98.4	786	2 Q6IU06_THELA	Q6IU06 thermomyces
2	3216	79.8	1632	2 Q4X048_ASPFU	Q4X048 aspergillus
3	3168	78.6	1630	2 Q5AVY3_LEMEU	Q5AVY3 aspergillus
4	2842	70.5	1962	2 Q78784_NEUCR	Q78784 neurospora
5	2814.5	69.8	1087	2 Q86292_GIBMO	Q86292 gibberella
6	2773	68.8	1814	2 Q4HXW9_GIBZE	Q4HXW9 gibberella
7	2761.5	68.5	1793	2 Q86292_GIBMO	Q86292 gibberella
8	2721	67.5	1666	2 Q862A3_COCHI	Q862A3 cochliobolus
9	2634	65.4	1519	2 Q2UE08_ASPOR	Q2UE08 aspergillus
10	1957.5	48.6	1676	2 Q4P0W2_USITVA	Q4P0W2 usitlago ma
11	1957.5	48.6	1676	2 Q8TG36_USITVA	Q8TG36 usitlago ma
12	1932.5	48.0	1556	2 Q55246_CRYNE	Q55246 cryptococcus
13	1895	47.0	1556	2 Q5KNG1_CRYNE	Q5KNG1 cryptococcus
14	1691	42.0	1153	2 Q4VXC3_HUMAN	Q4VXC3 homo sapien
15	1683.5	41.8	1797	2 Q4P9M8_HUMAN	Q4P9M8 homo sapien
16	1680.5	41.7	1770	2 Q4VXC5_HUMAN	Q4VXC5 homo sapien
17	1677	41.6	1161	2 Q8J1X1_BRARE	Q8J1X1 brachydanio
18	1676.5	41.6	1783	2 Q4R9M7_HUMAN	Q4R9M7 homo sapien
19	1673.5	41.5	1809	2 Q4R9M9_HUMAN	Q4R9M9 homo sapien
20	1673	41.5	1478	2 Q4LE42_HUMAN	Q4LE42 homo sapien
21	1672	41.5	1698	2 Q6TA13_MOUSE	Q6TA13 mus musculu
22	1670	41.4	1679	2 Q7PHR1_ANOCA	Q7PHR1 anopheles g
23	1669.5	41.4	1690	2 Q53T78_HUMAN	Q53T78 homo sapien
24	1669.5	41.4	1690	2 Q2NKA0_HUMAN	Q2NKA0 homo sapien
25	1669.5	41.4	1816	2 KIF1B_HUMAN	Q60333 mus musculu
26	1669	41.4	937	2 Q5XK63_MOUSE	Q5XK63 mus musculu
27	1669	41.4	1100	1 KIF1C_MOUSE	Q65071 mus musculu
28	1668.5	41.4	1689	2 Q6PSH4_MOUSE	Q6PSH4 mus musculu
29	1668.5	41.4	1698	2 Q3UHI6_MOUSE	Q3UHI6 mus musculu
30	1668.5	41.4	1816	2 Q4VXC6_HUMAN	Q4VXC6 homo sapien
31	1668.5	41.4	1823	2 Q4VXC4_HUMAN	Q4VXC4 homo sapien

32	1667.5	41.4	1816	1 KIF1B_RAT	O88658 rattus norv
33	1667	41.4	1103	1 KIF1C_HUMAN	O43896 homo sapien
34	1667	41.4	1120	2 Q6A011_MOUSE	O6A011 mus musculu
35	1665	41.3	1103	2 Q5U618_HUMAN	Q5U618 homo sapien
36	1663.5	41.3	1690	1 KIF1A_HUMAN	Q12756 homo sapien
37	1663.5	41.3	1695	1 KIF1A_MOUSE	P33173 mus musculu
38	1660.5	41.2	1816	1 KIF1B_MOUSE	O60575 mus musculu
39	1659	41.2	1100	2 Q8V189_MOUSE	O8V189 mus musculu
40	1657.5	41.1	628	2 Q3UY61_MOUSE	Q3UY61 mus musculu
41	1630.5	40.5	1671	2 Q9NBU1_DROME	Q9NBU1 drosophila
42	1629	40.5	1670	2 Q8MLF6_DROME	Q8MLF6 drosophila
43	1617	40.1	1097	1 KIF1C_RAT	Q35787 rattus norv
44	1611	40.0	1576	2 Q61G13_CAEBR	Q61G13 caenorhabdi
45	1590.5	39.5	1584	1 UN104_CAEBL	P23678 caenorhabdi

ALIGNMENTS

RESULT 1	ID	Q6IU06_THELA	PRELIMINARY;	PRT;	786 AA.
AC	Q6IU06;				
DT	05-JUL-2004,	integrated into uniprotKB/TREMBL.			
DT	07-FEB-2006,	entry version 10.			
DE	Unc104/KIF1A-like protein (Fragment).				
OS	Thermomyces lanuginosus (Humicola lanuginosa).				
OC	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.				
OX	NCBI_TaxID=5541;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Rivera S.B., Koch S.J., Bauer J.M., Edwards J.M., Bachand G.D.;				
RL	Submitted (May-2004) to the EMBL/GenBank/DBJ databases.				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
CC	Distributed under the Creative Commons Attribution-NonCommercial License				
CC	-----				
DR	EMBL: AY623608; AAT39887.1; -; mRNA.				
DR	GO; GO:0003874; C:mitochondrion; IEA.				
DR	GO; GO:0005875; C:mitochondrion associated complex; IEA.				
DR	GO; GO:0005524; F:ATP binding; IEA.				
DR	GO; GO:0003777; F:mitochondrion motor activity; IEA.				
DR	GO; GO:0000166; F:nucleotide binding; IEA.				
DR	GO; GO:0007018; F:mitochondrion-based movement; IEA.				
DR	InterPro: IPR001253; FHA.				
DR	InterPro: IPR001752; kinesin_motor.				
DR	Pfam: PF00498; FHA; 1.				
DR	Pfam: PF00225; Kinesin; 1.				
DR	PRINTS; PR00380; KINESINHEAVY.				
DR	SMART; SM00129; KISC; 1.				
DR	PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.				
DR	PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.				
KW	ATP-binding; Microtubule; Motor protein; Nucleotide-binding.				
FT	NON TER 786				
SQ	SEQUENCE 786 AA; 87201 MW; A008023FBAA70512 CRC64;				
QY	Query Match	98.4%;	Score 3966;	DB 2;	Length 786;
QY	Best Local Similarity	98.9%;	Pred. No. 4,6e-194;		
QY	Matches 775;	Conservative	2;	Mismatches 7;	Indels 0;
QY				Gaps 0;	
QY	1	MSGGGNIKVVVRVPRNAREIDRGACIVRMENQITLTPPGAERKARKSGKTINDGPK 60			
QY	1	MSGGGNIKVVVRVPRNAREIDRGACIVRMENQITLTPPGAERKARKSGKTINDGPK 60			
QY	61	AFAFDKSYSPDKAPVYARQEDLPDGLVPLLDNAFKGYNCCIFAYGGTSGSKSYSMWG 120			
QY	61	AFAFDKSYSPDKAPVYARQEDLPDGLVPLLDNAFKGYNCCIFAYGGTSGSKSYSMWG 120			
QY	121	YGEHGVIVRICODMFRRIINELOKDKNLTCYVAVSYLTIYNERVRLDLPSTYGNLKVRB 180			
QY	121	YGEHGVIVRICODMFRRIINELOKDKNLTCYVAVSYLTIYNERVRLDLPSTYGNLKVRB 180			

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OY 181 HPSTGYPVEDLAKLVVRSFOEINLMDENKARKATVAATNMNETSSRSHAVFTLTLOKMH 240
DB 181 HPSTGYPVEDLAKLVVRSFOEINLMDENKARKATVAATNMNETSSRSHAVFTLTLOKMH 240
OY 241 DEETKMDTEKVKAKISLVDLAGSERATSTGATGARLKEGAENINSLSTLGRVIAALADMSS 300
DB 241 DEETKMDTEKVKAKISLVDLAGSERATSTGATGARLKEGAENINSLSTLGRVIAALADMSS 300
OY 301 GKOQKQOLVPRYSVLTWLLKOSLGNSMTAMIAISPADINEEFTLSTLRVDSAKRIK 360
DB 301 GKOQKQOLVPRYSVLTWLLKOSLGNSMTAMIAISPADINEEFTLSTLRVDSAKRIK 360
OY 361 NHAVNEDPNARMIRLKEBLAQLRSKLQSSGGGAGAGSGGPPVEESYPPTPLEKOIV 420
DB 361 NHAVNEDPNARMIRLKEBLAQLRSKLQSSGGGAGAGSGGPPVEESYPPTPLEKOIV 420
OY 421 STQOPDATYKKSKEIYEQLNQSEKLYRDNLQNTWEKLAKEEIHKEERALEELGISI 480
DB 421 STQOPDATYKKSKEIYEQLNQSEKLYRDNLQNTWEKLAKEEIHKEERALEELGISI 480
OY 481 EKGFPVPRYSKEMPHLVNLSDDPLAECLVYNIKPGOTRGNVNOPTQAEIRLNGSKILK 540
DB 481 EKGFPVPRYSKEMPHLVNLSDDPLAECLVYNIKPGOTRGNVNOPTQAEIRLNGSKILK 540
OY 541 ECHTEFENVNVTVIVNEKAAVWVNGVRIDKPTRLSGRIILGDPHIFRPNHPEERABE 600
DB 541 ECHTEFENVNVTVIVNEKAAVWVNGVRIDKPTRLSGRIILGDPHIFRPNHPEERABE 600
OY 601 ROEOGSLRHSVTNSQLGSPAPGPHDRTLSKAGSDADGDSRSDSPHPFGKSDWIFYARR 660
DB 601 ROEOGSLRHSVTNSQLGSPAPGPHDRTLSKAGSDADGDSRSDSPHPFGKSDWIFYARR 660
OY 661 EASASALIGDOKISHLTDELALFPDVKARAVRGVLVEDNDSOSGSPFRDXYMSN 720
DB 661 EASASALIGDOKISHLTDELALFPDVKARAVRGVLVEDNDSOSGSPFRDXYMSN 720
OY 721 GTINDFSLDTALTPTGTPRSDDGDLFPFGDKSKODASVNDVEELRQOQAEALAKTA 780
DB 721 GTINDFSLDTALTPTGTPRSDDGDLFPFGDKSKODASVNDVEELRQOQAEALAKTA 780
OY 781 KOEF 784
DB 781 KOEF 784

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RA Penava M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,
RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Roming C.M., Ruter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Arai K.,
RA Machida M., Hall N., Barrett B.G., Denning D.W.,
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus".
RL Nature 438:1151-1156(2005).
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC Distributed under the Creative Commons Attribution-NonCommercial license
CC -----
DR EMBL; AAHP01000001; EAL93767.1; -, Genomic DNA.
DR GO; GO:0005875; C:mitochondrion associated complex; IEA.
DR GO; GO:0005524; F:AMP binding; IEA.
DR GO; GO:0003777; F:mitochondrion motor activity; IEA.
DR GO; GO:0007018; F:mitochondrion-based movement; IEA.
DR InterPro; IPR001752; Kinesin_motor.
DR InterPro; IPR001849; PH.
DR InterPro; IPR01993; PH_type.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00225; Kinesin; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
DR PROSITE; PS50003; PH_DOMAIN1; 1.
KW Complete proteome.
SQ SEQUENCE 1632 AA; 182726 MW; 1CAED6825E77444D CRC64;

Query Match 79.8%; Score 3216; DB 2; Length 1632;
Best Local Similarity 78.6%; Pred. No. 2.5e-155;
Matches 636; Conservative 68; Mismatches 73; Indels 33; Gaps 8;

OY 3 GCGNIKVVVRVRFNAREIDRGAKCIVRMEGNQTLTPPPGAEBARKS-GKTINDGPKA 61
DB 5 GCGNIKVVVRVRFNAREIDRGAKCIYOMKNGTLLVPPGADKSRKAGGAVGEPRT 64
OY 62 PAFDRSYSPDKAENYARQEDLPDGLGYPLIDNAFKGYNNCTFYAGTSGSKSYSMNGY 121
DB 65 PAFDRSYSPDKAENYARQEDLPDGLGYPLIDNAFKGYNNCTFYAGTSGSKSYSMNGY 124
OY 122 GKEHGVIPRICODMFRRLNELOKDKNLCTVSVSYLEIYNERVRLDLPSTGKLVREH 181
DB 125 GKEYGVIPRICODMFRRLNELOKDKNLCTVSVSYLEIYNERVRLDLPSTGKLVREH 184
OY 182 PSTGYPVEDLAKLVVRSFOEINLMDENKARKATVAATNMNETSSRSHAVFTLTLOKMH 241
DB 185 PSTGYPVEDLAKLVVRSFOEINLMDENKARKATVAATNMNETSSRSHAVFTLTLOKMH 244
OY 242 BETKMDTEKVKAKISLVDLAGSERATSTGATGARLKEGAENINSLSTLGRVIAALADMSSG 301
DB 245 BETKMDTEKVKAKISLVDLAGSERATSTGATGARLKEGAENINSLSTLGRVIAALADMSSG 304
OY 302 KOKKQOLVPRYSVLTWLLKOSLGNSMTAMIAISPADINEEFTLSTLRVDSAKRIK 361
DB 305 KOKKQOLVPRYSVLTWLLKOSLGNSMTAMIAISPADINEEFTLSTLRVDSAKRIK 364
OY 362 HAVVNEDPNARMIRLKEBLAQLRSKLQSSGGGAGAGSGG-PVEESYPPTPLEKOIV 420
DB 365 HAVVNEDPNARMIRLKEBLAQLRSKLQSSGGGAGAGSGG-PVEESYPPTPLEKOIV 420
OY 421 STQOPDATYKKSKEIYEQLNQSEKLYRDNLQNTWEKLAKEEIHKEERALEELGISI 480
DB 421 STQOPDATYKKSKEIYEQLNQSEKLYRDNLQNTWEKLAKEEIHKEERALEELGISI 480

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QY 481 EKGFGVPSKEMPHLVNLSDDPLLAECCLVYNIKPQTRGVNVOPTQAEIRLNGSKILK 540
D 481 EKGFGVSTGPKMPHVLNLSDDPLLAECCLVYNIKPQTTGNGMGSHVEIRLNGSKILP 540
QY 541 ECHTFENVNVVTVIVNEKAAMVNGVRIDKPTRLRSGYRIIIGDHFIFRPNHPEARAE 600
D 541 NHCFFENVNVVTVIVNEKAAMVNGVRIDKPTRLRSGYRIIIGDHFIFRPNHPEARAE 600
QY 601 ROESQILRHSVTNSQSGSPAPGR-HDRTLKAGSDAGD--SRSDSLPHFRGDSMPFYA 658
D 601 RVEOSILRHSVTNSQSGSPAPGR-HDRTLKAGSDAGD--SRSDSLPHFRGDSMPFYA 660
QY 659 RREAASAILGLDQKISHLTDELDALEFDYQKAAVARGLVENEDSDSSQSPFPRDKYM 718
D 661 RREAASAILGLDQKISHLTDELDALEFDYQKAAVARGLVENEDSDSSQSPFPRDKYM 719
QY 719 SNGTIDNFSLDITAITMGPTRSDGDPALFFGD--KKSIRQD----- 757
D 720 SNGTIDNFSLDITAITMGPTRSDGDPALFFGD--KKSIRQD----- 779
QY 758 --ASNVDELROQAQMEALKTAKQEF 784
D 780 AEAASDDADDELRLKEKMEBALRSTKEY 808

RESULT 3
OSAVY3_EMENT PRELIMINARY; PRT; 1630 AA.
AC OSAVY3;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DE Hypothetical protein.
GN ORFNames=AN7547.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RC NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RP STRAIN=FGSC 4;
RX PubMed=16372000; DOI=10.1038/nature04341;
RA Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
RA Batzoglou S., Lee S.-I., Bastenmeier M., Spevak C.C., Glueckebueck J.,
RA Kapitonov V., Jurka J., Scanzonchio C., Farman M., Butler J.,
RA Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Entfert C.,
RA Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
RA Doonan J.H., Yu J., Vilenken K., Pain A., Freitag M., Selker E.U.,
RA Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,
RA Kumagai T., Asai K., Machida M., Niernan W.C., Denning D.W.,
RA Caddick M., Hynes M., Paolacci M., Fischer R., Miller B.L., Dyer P.S.,
RA Sachs W.S., Osmann S.A., Birren B.W.;
RT "Sequencing of Aspergillus nidulans and comparative analysis with A.
RT fumigatus and A. oryzae."
RL Nature 438:1105-1115(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
EMBL: AACD01000129; EAA62127.1; -; Genomic DNA.
DR GO; GO:0005875; C: microtubule associated complex; IEA.
DR GO; GO:0005524; F: ATP binding; IEA.
DR GO; GO:0003777; F: microtubule motor activity; IEA.
DR GO; GO:0007018; F: microtubule-based movement; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR001752; kinesin_motor.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH_type.
DR Pfam; PF00498; FHA; 1.
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DR Pfam; PF00225; kinesin; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR Hypothetical protein_
SQ SEQUENCE 1630 AA; 182784 MW; 85AD0AF238645F9D CRC64;

Query Match 78.6%; Score 3169; DB 2; Length 1630;
Best Local Similarity 78.0%; Pred. No. 7.1e-153;
Matches 627; Conservative 73; Mismatches 78; Indels 26; Gaps 10;

QY 3 GGGNIKVVAVRVPFNPAEIRDRGAKCTVRMEGNGTITLPPGAEEKARKSG-KITMDGPKA 61
D 5 GGGNIKVVAVRVPFNPAEIRDRGAKCTVRMEGNGTITLPPGAEEKARKSG-KITMDGPKA 64
QY 62 FAFDRSYWSPDKAAPYARQEDLFODLGVPLNNAFGYNNCFAYGQTSQSGSYMMGY 121
D 65 FAFDRSYWSPDKAAPYARQEDLFODLGVPLNNAFGYNNCFAYGQTSQSGSYMMGY 124
QY 122 GKEHGYIPRICQDFRINELQDKNLCTVEVSYLEIYNERVRLNPSKGNLKYREH 181
D 125 GKEHGYIPRICQDFRINELQDKNLCTVEVSYLEIYNERVRLNPSKGNLKYREH 184
QY 182 PSTGPIVEDIAKLVRSFOEINLMDGKARTVAATNNMETSSRSHAVFTLTQKMD 241
D 185 PSTGPIVEDIAKLVRSFOEINLMDGKARTVAATNNMETSSRSHAVFTLTQKMD 244
QY 242 EETKMTKAKAKIQLVDLGSERATSGATGATKGAETNRSLTGRVIALADWSSG 301
D 245 AETSMDEKVSRLVDLGSERANSTGATGATKGAETNRSLTGRVIALADWSSG 304
QY 302 KQKQNLVPRDSVLTMLKDSLGNSMTAMIAISPADINFEETLSTLRVYASAKRIK 361
D 305 K-KKQGVPRDSVLTMLKDSLGNSMTAMIAISPADINFEETLSTLRVYASAKRIK 363
QY 362 HAVNEDPNAIRIRLKEBELAQIRSKLQSSGGGAGGAGGV-EEYPPDTPLEKQIV 420
D 364 HAVNEDPNAIRIRLKEBELAQIRSKLQSSGGGAGGAGGV-EEYPPDTPLEKQIV 423
QY 421 STQPPDPAVYKSKAIVQLNQSSEKLYKDLQNTWEKLAKEEIKERPAALEEGIST 480
D 424 STQPPDPAVYKSKAIVQLNQSSEKLYKDLQNTWEKLAKEEIKERPAALEEGIST 483
QY 481 EKGFGVPSKEMPHLVNLSDDPLLAECCLVYNIKPQTRGVNVOPTQAEIRLNGSKILK 540
D 484 EKGFGVSTGPKMPHVLNLSDDPLLAECCLVYNIKPQTTGNGMGSHVEIRLNGSKILA 543
QY 541 ECHTFENVNVVTVIVNEKAAMVNGVRIDKPTRLRSGYRIIIGDHFIFRPNHPEARAE 600
D 544 ECHTFENVNVVTVIVNEKAAMVNGVRIDKPTRLRSGYRIIIGDHFIFRPNHPEARAE 603
QY 601 ROESQILRHSVTNSQSGSPAPGR-HDRTLKAGSDAGD--SRSDSLPHFRGDSMPFYA 658
D 604 RVEOSILRHSVTNSQSGSPAPGR-HDRTLKAGSDAGD--SRSDSLPHFRGDSMPFYA 662
QY 659 RREAASAILGLD-QKISHLTDELDALEFDYQKAAVARGLVENEDSDSSQSPFPRDKY 717
D 663 RREAASAILGLD-QKISHLTDELDALEFDYQKAAVARGLVENEDSDSSQSPFPRDKY 720
QY 718 MSGTIDNFSLDITAITMGPTRSDGDPAL-----FFGDKKSQKODAS-N 760
D 721 MSGTIDNFSLDITAITMGPTRSDGDPAL-----FFGDKKSQKODAS-N 780
QY 761 VVVEELRQQAQMEALKTAKQEF 784
D 781 QGIDELRSEKARMEALRVAKEY 804

RESULT 4
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075784_NEUCR
 ID 075784_NEUCR PRELIMINARY; PRT; 1962 AA.
 AC 125784;
 DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
 DT 15-DEC-2003, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Hypothetical protein.
 DE ORFNames=NCU06733.1;
 GN Neurospora crassa.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxId=5141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [large scale genomic DNA].
 RC STRAIN=74-OR23-1A / FGSC 987; DOI=10.1038/nature01554;
 RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
 RA Werner-Washburne M., Selitrenikoff C.P., Kinsey J.A., Brann E.L.,
 RA Zeller A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
 RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
 RA Stange-Thomann N., Barrett R., Gnerre S., Kamai M., Kamysasellis M.,
 RA Maccelli E., Bielke C., Rudd S., Fishman D., Krystofova S.,
 RA Madsen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,
 RA Macino G., Carcheside D.E.A., Li W., Prater R.J., Omani S.A.,
 RA Desouza C.C., Glass N.U., Orbach M.J., Berglund J.A., Voelker R.,
 RA Varden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.W.,
 RA "The genome sequence of the filamentous fungus *Neurospora crassa*.";
 RL Nature 422:859-868(2003).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
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 CC -----
 CC EMBL; AABX0100301; EAAJ1425.1; -; Genomic DNA.
 CC
 DR HSSP; P33173; 1158.
 DR GO; GO:0005875; C:microtubule associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:microtubule motor activity; IEA.
 DR GO; GO:0007018; F:microtubule-based movement; IEA.
 DR InterPro; IPR000253; FHA.
 DR InterPro; IPR001752; kinesin_motor.
 DR InterPro; IPR01849; PH.
 DR InterPro; IPR011993; PH_type.
 DR Pfam; PF00498; FHA; 1.
 DR Pfam; PF00225; Kinesin; 1.
 DR Pfam; PF00169; PH; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00240; FHA; 1.
 DR SMART; SM00129; KISC; 1.
 DR SMART; SM00233; PH; 1.
 DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR Hypothetical protein.
 KW SEQUENCE 1962 AA; 214863 MW; 180ADB5E87634D4 CRC64;
 Query Match 70.5%; Score 2842; DB 2; Length 1962;
 Best Local Similarity 71.2%; Pred. No. 4.1e-136;
 Matches 581; Conservative 71; Mismatches 118; Indels 46; Gaps 11;
 QY 1 MSGGGNIKVVVRPARNAREIDGAKCTIRMESGNOTIILPPPGAEKARKSGKTINDGPK 60
 DB 8 MSGGGNIKVVVRPARNAREIDGAKCTIRMESGNOTIILPPPGAEKARKSGKTINDGPK 62
 QY 61 AFAFDRSYWSPDKNAPNVAQDQLHEDLGFLLDNAFGKYNNCIFAYGQTGSGKSYMWG 120
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DB 63 IFAPDRSYWSPDKNAPNVAQDQLHEDLGFLLDNAFGKYNNCIFAYGQTGSGKSYMWG 122
 QY YGKEHGVPRICODMFRINELQKDNLTCTVEVSYLTYVERVVDLINPSTKGLKYRE 180
 DB 123 YGKDGILLPMICODMFKIINDQDNLRCTVEVSYLTYVERVVDLINPARKGLKYRE 182
 QY 181 HPSGTPIYEDLAKLVRSFOEIEINLMDGNKARTVAATNMNETSSRSHAVFTLLTKRM 240
 DB 183 HPSGTPIYEDLAKLVRSFOEIEINLMDGNKARTVAATNMNETSSRSHAVFTLLTKRM 242
 QY 241 DEETMDTEKVAKISLVLDLAGSERATSGATGARLKEGAEINRSISTGRVYALADMS 300
 DB 243 DEETMDTEKVAKISLVLDLAGSERATSGATGARLKEGAEINRSISTGRVYALADMS 302
 QY 301 GKQKKNQ---VPYDSVLTWMLKDSLGNSMTAAIISPADINFEETLSTRVADSAS 357
 DB 303 GKQKKNQSAAGQVPYDSVLTWMLKDSLGNSMTAAIISPADINFEETLSTRVADSAS 362
 QY 358 RIKNAAVNEDPNAMIRELKEELALQRLSKLQSSGSGGAGGSGGPGVEESYPPDTPLEK 417
 DB 363 RIKNAAVNEDPNAMIRELKEELALQRLSKLQSSGSGGAGGSGGPGVEESYPPDTPLEK 418
 QY 418 QIVSIQDPATVKKSKAEIYQNLQNSKLYRDLNQTEBEKLAKTEBIHKREALBELG 477
 DB 419 QIVSIQDPATVKKSKAEIYQNLQNSKLYRDLNQTEBEKLAKTEBIHKREALBELG 478
 QY 478 ISEKGFPGPHSKEMPHLVNLSDDPLAECLVYNIKPGQVRGVN---NODTQAEIRLNG 535
 DB 479 ISEKGFPGPHSKEMPHLVNLSDDPLAECLVYNIKPGQVRGVN---NODTQAEIRLNG 538
 QY 536 SKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLSGYRIILGDFHFRFNP 594
 DB 539 SKILKEHCTFENVDNVVTIVPNEKAAVMVNGVRIDKPTRLSGYRIILGDFHFRFNP 598
 QY 595 EBARER---OEGSLRHSVTNSOLG-----SPAPGRHDTLSQAGDADDSDD 642
 DB 599 LEAKERARERAOQSLRQSLRQSLRQSLRQSLRQSLRQSLRQSLRQSLRQSLRQSLR 656
 QY 643 SPLPHFRG-KQSDMYARREASATILGDKISHLTDELDPDQVQKARVARGLYVD 701
 DB 657 SPAPSRRTKESDWSFARREAGAILGTQNFATKLTDELDPDQVQKARVARGLYVD 716
 QY 702 NEDSDQSGSPYRDYRNGTIDNFSLDPAITMPCPTPRSDDDGAL----- 747
 DB 717 DDIDISMASYPYRREXLYSTGLTIDNFSLDPAITMPCPTPRSDDDGAL----- 776
 QY 748 --FPGDKSKQDASVDVBEILFQQAQMEALKTAK 781
 DB 777 KEKYDQDKTAEEAANVAVEIEIKERARMEETLMQK 812
 RESULT 5
 ID Q86292_GIBMO PRELIMINARY; PRT; 1087 AA.
 AC Q86292;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Kinesin.
 GN Name=KLE8;
 OS Gibberella moniliformis (Fusarium verticillioides).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
 OX NCBI_TaxId=117187;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22627967; PubMed=12742059; DOI=10.1016/S1087-1845(03)00022-7;
 RA Schoch C.L., Aist J.R., Yoder O.C., Gillian Turgeson B.,
 RT "A complete inventory of fungal kinesins in representative filamentous
 fungi.";
 RL Fungal Genet. Biol. 39:1-15(2003).
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 CC EMBL: AY330444; AA059306.1; -; Genomic_DNA.
 DR HSSP: P33173; 1155.
 DR GO: GO:0005874; C:microtubule; IEA.
 DR GO: GO:0005875; C:microtubule associated complex; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0003777; F:microtubule motor activity; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR GO: GO:0007018; F:microtubule-based movement; IEA.
 DR InterPro: IPR001253; FHA.
 DR Pfam: PF00498; FHA; 1.
 DR Pfam: PF00225; Kinesin; 1.
 DR PRINTS: PRO0380; KINESINHEAVY.
 DR SMART: SM00129; KISC; 1.
 DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE: PS50067; KINESIN MOTOR DOMAIN2; 1.
 DR ATP-binding; Microtubule; Motor protein; Nucleotide-binding.
 SQ SEQUENCE 1087 AA; 120899 MW; B8F19ADB309C4D5 CRC64;
 Query Match 69.8%; Score 2814.5; DB 2; Length 1087;
 Best Local Similarity 70.3%; Pred. No. 4.6e-135;
 Matches 575; Conservative 82; Mismatches 112; Indels 49; Gaps 14;
 QY 2 SGGGNKKVVVRVPPNAREIDRGAKCTVMEGNOTITPPGABEKARKSGKTIIMGPKA 61
 DB 4 TGGGNNKVVVRCPSPNSREIERAKCTVMEGNOTITVTAEG--KGVKGG--GPKA 55
 QY 62 FAFDRSYWFFDKNAPNYARQEDLFODLGVPLLDNAFFGYNCCI FAYGQTSGSKSYMWGY 121
 DB 56 FAFDRSYWFFDKNAPNYARQEDLFODLGVPLLDNAFFGYNCCI FAYGQTSGSKSYMWGY 115
 QY 122 GKSHGVIPIRCQMFRRINELQOKNLCTVEVSYLEYINERVRDLINPSTKGNLKYREH 181
 DB 116 GKSHGVIPIRCQMFRRINELQOKNLCTVEVSYLEYINERVRDLINPSTKGNLKYREH 175
 QY 182 PSTGPIVEDAKLVVVSFOEINLMDEGNKAFVATANNMETSRSRAVFTLLTQKMD 241
 DB 176 PSTGPIVEDAKLVVVSFOEINLMDEGNKAFVATANNMETSRSRAVFTLLTQKMD 235
 QY 242 EETKMDTEKVAKISLVDLGSEKATSGATGARLKEGAEINRSLSLTVGRVIALADMSG 301
 DB 236 ADTKMEKVAKISLVDLGSEKATSGATGARLKEGAEINRSLSLTVGRVIALADMSG 225
 QY 302 KQKKNQL--VPYDSVLTWLLKQSLGNSMTAMIAISPADINFEETSLTRYAASAKRI 359
 DB 296 GKXKKGSTGVPRYDSVLTWLLKQSLGNSMTAMIAISPADINFEETSLTRYAASAKRI 355
 QY 360 KNNAAVNEDPNAMITELKEELAQLSKLOSGGGGGGAGSGGPVEBSYPPPTPEKQI 419
 DB 356 KNNAAVNEDPNAMITELKEELAQLSKLOSGGGGGGAGSGGPVEBSYPPPTPEKQI 414
 QY 420 VSIQCPDATVKKMSKAEIVQLNQSEKLYRDLNQTEBEKLAETKEIHKEREALTEEGIS 479
 DB 415 VSIQCPDATVKKMSKAEIVQLNQSEKLYRDLNQTEBEKLAETKEIHKEREALTEEGIS 474
 QY 480 IEKGVGYPHSKMPLVNLSDPDLAECVLVNIKPGQTRVGNV--NODTQAEIRLNGSK 537
 DB 475 IEKGVGYPHSKMPLVNLSDPDLAECVLVNIKPGQTRVGNV--NODTQAEIRLNGSK 534
 QY 538 ILEKHTCFENV--DNVTVIPNEKAAVMNVCVRIDKTRLSRGYRIILGPHIRRNHPEP 596
 DB 535 ILEKHTCFENV--DNVTVIPNEKAAVMNVCVRIDKTRLSRGYRIILGPHIRRNHPEP 594
 QY 597 ARAEROE-----QSLRHSVTNSQL-----GSPAPG--RHDRTLKAGSDADGDSRDS 643
 DB 595 ARAERAEVERPERGSLRHSITASQLADLRGSPSPSPRPHERSFRAVSEFG--ISRPES 653
 QY 644 PLPHFR--GSDSWFYARRRASAAILGLDQKISHLTDELDALFDYDQKARAVRGIVEDN 702
 DB 654 PSIFORSGRESDSLARRRAGAAILGSDQSLTSLTDEINLAFEDVQARAAR---VNGR 710

QY 703 ED-SDSOSPVPVQKXMSNCTINDFSLDPAITMPTGRSDDDGAL----- 747
 DB 711 EDGDDSESSYPIDKXTLSNCTMDNFSLDALIMPSTPKQSGPDDRLKEVREELQNRLKEQ 770
 QY 748 --FFGDKKSKODASNVDEELRQQAQMEAEALTAQOE 783
 DB 771 KEQYQQLMSAEANVIEIKQEKYKMEALKEKED 808
 RESULT 6
 ID 086ZB4_BOTCI PRELIMINARY; PRT; 1814 AA.
 AC 086ZB4;
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003, sequence version 1.
 DT 07-FEB-2006, entry version 17.
 DE kinesin.
 GN Name=KLP8;
 OS Botrytis cinerea (Noble rot fungus) (Botryotinia fuckeliana).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
 OC Helotiales; Sclerotiniaceae; Botryotinia.
 OX NCBI_TaxID=40559;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=2627967; PubMed=12742059; DOI=10.1016/S1087-1845(03)00022-7;
 RA Schoch C.L., Aist J.R., Yoder O.C., Gillian Turgon B.,
 RT "A complete inventory of fungal kinesins in representative filamentous
 ascomycetes.";
 RL Fungal Genet. Biol. 39:1-15(2003).
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 CC EMBL: AY330422; AA059284.1; -; Genomic_DNA.
 DR HSSP: P33173; 1155.
 DR GO: GO:0005875; C:microtubule associated complex; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0003777; F:microtubule motor activity; IEA.
 DR GO: GO:0007018; F:microtubule-based movement; IEA.
 DR InterPro: IPR001253; FHA.
 DR InterPro: IPR001752; kinesin_motor.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR011993; PH_type.
 DR Pfam: PF00498; FHA; 1.
 DR Pfam: PF00225; Kinesin; 1.
 DR PRINTS: PRO0380; KINESINHEAVY.
 DR SMART: SM00129; KISC; 1.
 DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE: PS50067; KINESIN MOTOR DOMAIN2; 1.
 DR PROSITE: PS50067; PH DOMAIN; 1.
 SQ SEQUENCE 1814 AA; 201181 MW; 5F989F1BF2622BA1 CRC64;
 Query Match 68.8%; Score 2773; DB 2; Length 1814;
 Best Local Similarity 72.7%; Pred. No. 1.2e-132;
 Matches 575; Conservative 63; Mismatches 105; Indels 48; Gaps 14;
 QY 31 MEGNQTILTPPGABEKAR--KSGKTIIMGPAPAFADRSYWFDDKKAAPNYARQEDLFODL 88
 DB 1 MKDAQTVITPPGHEKSKSDAKGKA--DTGQVFAFADRSYWFDDKNDPSYACQDNHTDL 59
 QY 89 GVPPLDNAFGYNNCIFAAYGQTSGSKSYMWGYGKHEGVIPIRCQMFRRINELQOKNL 148
 DB 60 GVPPLDNAFGYNNCIFAAYGQTSGSKSYMWGYGKDAVYIPRICQMFRRIGELQODKHL 119
 QY 149 TCTVEVSYLEYINERVRDLINPSTKGNLKYREHPSGTVEDLAKLVVVSFOEINLMDE 208
 DB 120 KCTVEVSYLEYINERVRDLINPSTKGNLKYREHPSGTVEDLAKLVVVSFOEINLMDE 179
 QY 209 GKKARTVAATNNNETSSRSRAVFTLLTQKMDDEETKMDTEKVAKISLVDLGSEKATSG 268
 DB 180 GKKARTVAATNNNETSSRSRAVFTLLTQKMDDEETKMDTEKVAKISLVDLGSEKATSG 239

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QY 269 GATGARKKEGAEINRSLSTLGRVIALALADMSCKOKK-----NOLVYRDSVLTWLLKDSL 324
DB 240 GATGARKKEGAEINRSLSTLGRVIALALADMSCKKKVKQKQ--VYRDSVLTWLLKDSL 298
QY 325 GGNSTMTAMIAISPADINFEETSTLRVYDSAKRIQNHAVNEDPAARIMRELKEELAO 384
DB 299 GGNSTMTAMIAISPADINFEETSTLRVYDSAKRIQNHAVNEDPAARIMRELKEELAO 358
QY 385 RSKLOSSGGGGGAGSGGSPVEESYPPDTPLEKQIVSIOQPDATVKKMSKAEIVEOLNOS 444
DB 359 RSKLT--TGCGGWRGGS--PADEIVAEQTPLEKQMTIVISSDGAVKVSKAEITEQOLNOS 414
QY 445 EKLTYDNLNTWEKLAKTETEHKEREALAEELGISTEKGFPVGYHSEKMPHVLNLSDDPL 504
DB 415 EKLTYDNLNTWEKLAKTETEHKEREALAEELGISTEKGFPVGLHTPKMPLNLSDDPL 474
QY 505 LAECLVYNNIKPGQTRGVN--NQDQAEIRLNGSKILKEHCTEENVDNVTVIPEKAAV 562
DB 475 LAECLVYNNIKPGQSTSGVNDTNAHAAEIRLNCTRIHHECTEENVDNVTVITPTGAAV 534
QY 563 MNGVRIDKPTRLRSYRIILGDFHIFRPNHPEAPAEKOEOSLHSHVYTNSQL----- 616
DB 535 MNGQREKPTRLRSQFRVILGDFHIFRPNHPEAPAEKOEOSLHSHVYTNSQL----- 594
QY 617 -----GSPAGRHDTLSKAGSDA--DDDSRSDSPLPHFRGKDSDFYARPREASAILG 668
DB 595 DKFSPSSTRPA-HDFTFSKATSDLPDSDSRSDSPVPG-RGL-SWMSLARRRGAAGAILG 651
QY 669 LDQKISHLTDELDLAFDDVOKARAVRGVLVEDNEDSDSQSPFVADKYMSNTGIDNFSL 728
DB 652 TQOKIAGLSDEELNVLFEDVQARA-ERATANLEDDLSTVTSYPMREKTLNSNTLDNFSL 710
QY 729 DTAITMPTGPRSDDDGAL-----FFGDKKSQDASNVDFEELRQOQAO 772
DB 711 DTAITMPTGPRSDDDGAL-----FFGDKKSQDASNVDFEELRQOQAO 770
QY 773 MEALAKTAKOE 783
DB 771 MEETLEKVEE 781

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RESULT 7

Q4HXW9_GIBZE PRELIMINARY; PRT; 1793 AA.

16-AUG-2005, integrated into UniProtKB/TrEMBL.

07-FEB-2006, entry version 6.

Hypothetical protein.

ORFNames=FG10189.1;

Gibberella zeae (Fusarium graminearum).

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

NCBI_TaxID=5518;

NUCLEOTIDE SEQUENCE [Large scale genomic DNA].

STRAIN=PH-1 / NRRL 31084.

Birren B.W., Nussbaum C., Abouelleil A., Allen N., Anderson S., Archachl H.M., Barina N., Bastien V., Bloom T., Boguslavsky L., Bouhaghaler B., Butler J., Calvo S.E., Camarata J., Chang J., Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K., Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R., Eriksson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.E., Gardyna S., Gheirre S., Graham L., Grand-Pierre N., Hafez N., Hagoopian D., Hagoeb B., Hall J., Horton L., Hulme W., Iliev I., Jaffe C., Johnson R., Jones C., Kamal M., Kanat A., Kartas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A., Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J., Matthews C., Mauceli E., McCarthy M., Meldrum J., Menus L., Mitova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R., Nielsen C.B., Norbu K., O'Connor T., O'Donnell P., O'Neill D., Oliver J., Peterson K., Phunkhang P., Pierre N.,

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RA Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P., Roman J., Schuer S., Schupbach R., Seaman S., Severy P., Smitnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M., Talama J., Testaye S., Theodore J., Topham K., Travers M., Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B., Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M., Lander E.S.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAC010004.4; EAA70032.1; -; Genomic DNA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; F:microtubule-based movement; IEA.
DR InterPro; IPR001752; Kinesin_motor.
DR InterPro; IPR001849; PH.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00225; Kinesin; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
KW Complete proteome, Hypothetical protein.
SQ SEQUENCE 1793 AA; 198597 MW; 44AF342ED904207 CRC64;

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Query Match 68.5%; Score 2761.5; DB 2; Length 1793;
Best Local Similarity 68.8%; Pred. No. 4,7e-132;
Matches 564; Conservative 91; Mismatches 108; Indels 57; Gaps 16;

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QY 2 SGGGNIKYVVRVPRPNAREIDRGAKCYRMESGNTITLPPGAEEKAKSKGTIND-GRK 60
DB 4 AGGGNIKVVRCRPPNSRBIERNACIIVEMKGNQIVITAP-----EGGVADSGPK 54
QY 61 AFAFDSYWSFDKMPNPNYARQEDLFQDGVPLDLNAFGYNNCFAYGQTSKSGKSYNMG 120
DB 55 AFAFDSYWSFYKDDPNYAGSNLFDGQPLDPAFEGYNNCFAYGQTSKSGKSYNMG 114
QY 121 YGKEHGVIPRLIQDMFRRINELQDKNLCTYVESYLEIYNERVADLLNPSTKGLKYRE 180
DB 115 YGKEIGIVPMIQEIFKADDEIQDKGKTCTYVESYLEIYNERVADLLNPSTKGLKYRE 174
QY 181 HSTGTPYVEDLAKLVYRSFOETENLMDGKNKARTYAAATNMETSRSRAVFTLTQKWH 240
DB 175 HSTGTPYVEDLAKLVNFOETENLMDGKNKARTYAAATNMQTSRSRAVFTLTQKXI 234
QY 241 DEETQDTEKVAKISLVLDAGSERATSGATGARLKEGAETIRNSTLGRVIALALADMS 300
DB 235 DTDITMALEKAKISLVLDAGSERANSTGATGARLKEGAETIRNSTLGRVIALALADLS 294
QY 301 -GKQKNO-LVYRDSVLTWLLKDSLGNSMTAMIAISPADINFEETSTLRVYDSAKR 358
DB 295 PEKKKKSGQVYRDSVLTWLLKDSLGNSTMTAMIAAVSPADINFEETSTLRVYDSAKR 354
QY 359 IONHAVNEDPAARIMRELKEELALBRKLTSSGGGGGAGGS--GQVEESYPPDTPLE 416
DB 355 IONHAVNEDPAARIMRELKEELSLRLRKL-----GGGGGPGGAVVAG--ETVAGCTPLD 407
QY 417 KOIVSIQPDATVKKMSKAEIVEQJNOSEKLYRDLNQTWEKLAKTETEHKEREALAEEL 476
DB 408 QQVSIITGPDGVLTKVYSKAEIIEQJLSQSEKLLTDLNQTWEEKLKTETEHKEREALAEEL 467
QY 477 GISIEKFPVGYHSEKMPHVLNLSDDPLAECLVYNNIKPGQTRGVN--NQDQAEIRLN 534
DB 475 GISIEKFPVGYHSEKMPHVLNLSDDPLAECLVYNNIKPGQTRGVN--NQDQAEIRLN 534

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Db 468 GSIEKGVGLHTPKKPHLVNLSDDPLAECLVNLKPGTTGVGNVDINADHOANIRLN 527
Qy 535 GSKILKEHCTFEN-VDNVVTIVPNEKAAMVWNGVRIIDKPTLRSGYRIILGDFHIFRPNH 593
Db 528 GSRIILHDHCSFEAAADGVTTLTPSEGAASVWINKRIITEPQLSHSGRVILGDPHIFRPNH 587
Qy 594 PEFARAEKROE-----OSLRHSVTSNQL-----GSPAPG--RHDRTLSSAGSDADGDSR 640
Db 588 PHEARAEKRAEVPDRPQSLRLHSTITASQLQALDRGSPSPSPRPGHRSFSRSEFGD-ISR 646
Qy 641 SOSPLPHFR-GKSDMFYARREAAASAILGDKIKSHLTDELALFDVQKAAVNRGLV 639
Db 647 PEPSPISFQNRGRSDWSLARREAAAILGSDQNLTSLSDELNALFEEDVQKAAERVNVR 706
Qy 700 ENEDSDSOSQSPFVRDKYMSNGTIDNPSLDTAITMPTGTPRSDDDGAL----- 747
Db 707 EDGDDSD--SSYIRKRYLSNGTMDNPSLDTALTMSTPKQSEPDRLRREVLQNKLE 764
Qy 748 ---FFGDKKSKQDASNVDEELRQQAOMEEALKTKAKOE 783
Db 765 KOKEVEYQDOLKSAAANVEIEIKOEKRVKMEALQELKED 804

RESULT 8
Q86Z3 COCHE PRELIMINARY; PRT; 1666 AA.
ID Q86Z3 COCHE
AC Q86Z3
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Kinesin.
GN Name=KLP8;
OS Cochliobolus heterostrophus (Drechslera maydis).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5016;
RN NUCLEOTIDE SEQUENCE. Pubmed=12742059; DOI=10.1016/S1087-1845(03)00022-7;
RP MEDLINE=22627967; PubMed=12742059; DOI=10.1016/S1087-1845(03)00022-7;
RX Schoch C.L., Aist J.R., Yoder O.C., Gillian Turgeon B.,
RT "A complete inventory of fungal kinesins in representative filamentous
RL ascomycetes";
RL Fungal Genet. Biol. 39:1-15(2003).
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CC -----
CC EMBL; AY230433; AA059295.1; -; Genomic_DNA.
DR HSSP; P33173; 1158.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; F:microtubule-based movement; IEA.
DR InterPro; IPR001752; FHA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH_type.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00225; Kinesin; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
SQ SEQUENCE 1666 AA; 186129 MM; 9F58CCCCCF80F16EA CRC64;

Query Match 67.5%; Score 2721; DB 2; Length 1666;
Best Local Similarity 69.8%; Pred. No. 4.9e-130;
Matches 552; Conservative 77; Mismatches 116; Indels 46; Gaps 11;
Qy 31 MEGNQITLTPPPGAEBKARKSGKTINDGPAFAFDSSYMSFDPKGNAPVYARQEDLFDLGV 90

Db 65 MKGDQITLSPANTDVKG-KAAKAAEGVKTFAFDSYMSFDDAPRVAGQDNLHEDLGK 123
Qy 91 PLIDNAFKYNNICIFAYGOTSGSKSYMMGYGEHGVIPRICODMFRRIINELQDKNLTC 150
Db 124 PLIDNAFQGYNNICIFAYGOTSGSKSYMMGYGEHGVIPRICODMFRRIINELQDKNLTC 163
Qy 151 TVEVSYLIEYNERVRLDLPSTKGNLKVREHPSTGPVEDLAKLVYRSFOEINLDEGN 210
Db 184 TVEVSYLIEYNERVRLDLPSTKGNLKVREHPSTGPVEDLAKLVYRSFOEINLDEGN 243
Qy 211 KATVAATMNETSSSHAVFTLTQKHDEETKQDTEKVAKISLVDLAGESTGA 270
Db 244 KATVAATMNETSSSHAVFTLTQKHDEETKQDTEKVAKISLVDLAGESTGA 303
Qy 271 TGAIRKEGAEINRSLTLKRVIALALDMSGKQKNQVLVYRPSVLTWILKDSLGNSMT 330
Db 304 TGAIRKEGAEINRSLTLKRVIALALDMSGKQKNQVLVYRPSVLTWILKDSLGNSMT 361
Qy 331 AMIAAISPADINFEETLSTLRVADSARKIKNAHVNEDPVARMIRELKEBLAQRSKLG 390
Db 362 AMIAAISPADINFEETLSTLRVADSARKIKNAHVNEDPVARMIRELKEBLAQRSKLG 421
Qy 391 SGGGGGAGSGGSPVEESTPPTPLEKQIVSIQDPATVKKSKAEIVBOLNSEKLYRD 450
Db 422 GGGGGGAGSGGNGIVEQYPPDTPLEKQWISITQADGSTKYSKAEIAEQLTQSEKLYTE 481
Qy 451 LNTWEKLAKEIEIKEREAALEELGISTEGFVGPYHYSKEMPHLVNLSDDPLAECLV 510
Db 482 LNTWEKLAKEIEIKEREAALEELGISTEGFVGPYHYSKEMPHLVNLSDDPLAECLV 541
Qy 511 YNKPQTRGVNNOPTQ-AEIRLNGSKILKEHCTFENVNVTIVPNEKAAMVWNGVRI 569
Db 542 YNKPQTRGVNNOPTQ-AEIRLNGSKILKEHCTFENVNVTIVPNEKAAMVWNGVRI 601
Qy 570 DKPTRLSGYRIILGDPHIFRPNHPEARAEKROE-QSLRHSVTSNQLS-----PAPG 622
Db 602 DKPTRLSGYRIILGDPHIFRPNHPEARAEKROE-QSLRHSVTSNQLS-----PAPG 661
Qy 623 RHRH---TISKAGSDADGDS-RSDSPLPHFRGDSWMFARRRAAAILGDKIKSHLTD 678
Db 662 RHRH---TISKAGSDADGDS-RSDSPLPHFRGDSWMFARRRAAAILGDKIKSHLTD 720
Qy 679 DELDALFDVQKAAVNRG-----LVEDNEDSDSOSQSPFVRDKYMSNGTIDNPSLDTAIT 723
Db 721 EDPEALYEDLSRLRETRKARPESRMISDGDTSMSYPRREKYAAGTIDNPSLDTALT 780
Qy 734 MPTGPRSD-----DDGDLFFGDKKSKQDASNVDEELRQQAOM 773
Db 781 MPTGPRSD-----DDGDLFFGDKKSKQDASNVDEELRQQAOM 835
Qy 774 EEALTKAQEF 784
Db 836 QRQMKAKQEAFF 846

RESULT 9
Q2UE08 ASPOR PRELIMINARY; PRT; 1519 AA.
ID Q2UE08 ASPOR
AC Q2UE08
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE Kinesin-like protein.
GN ORFNames=AO090026000806;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=RIB 40;
RX Pubmed=16372010; DOI=10.1038/nature04300;

RA Machida M., Arai K., Sano M., Tanaka T., Kumagai T., Terai G.,
 RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
 RA Horuchi K., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
 RA Bhattacharjee D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,
 RA Hosoyama A., Ichinomiya M., Igasaki R., Iwashita K., Juvvuri P.R.,
 RA Kato M., Kato Y., Kim T., Kokubun A., Maeda H., Maeyama N.,
 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,
 RA Sakemoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
 RA Komori T., Koyama Y., Mihetoki T., Sunarnan S., Tanaka A., Isono K.,
 RA Kishimoto S., Ogasawara N., Kikuchi H.,
 RA "Genome sequencing and analysis of *Aspergillus oryzae*."
 RA Nature 438:1157-1161(2005).
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 CC EMBL, AP007159; BAE60207.1; -; Genomic DNA.
 DR SEQUENCE 1519 AA; 169635 MW; F0A56250F5859B6 CRC64;

Query Match 65.4%; Score 2634; DB 2; Length 1519;
 Best Local Similarity 67.7%; Pred. No. 1,2e-125; Indels 130; Gaps 9;

Matches 536; Conservative 58; Mismatches 68; Indels 130; Gaps 9;

3 GGGATKVVVRVPPNAREIDRGAKCIVRMGNTILTPPGAEEKARKS--GKTIWDGPK 60
 5 GGGATKVVVRVPPNAREIDRGAKCIVRMGNTILTPPGAEEKARKS--GKTIWDGPK 64
 61 AFAFDRSYWSPDKNAFNVARQEDLFQDLGVPLLDNAFKYNNCFAYGOTGSGKSYWVG 120
 65 TFAFDRSYWSPDKNAFNVARQEDLFQDLGVPLLDNAFKYNNCFAYGOTGSGKSYWVG 124
 121 YGKEGCVIPRIQODMFRINELQKKNLCTVEVSLTYNRYRPLLPSTGKNAKPE 180
 125 YGKEGCVIPRIQODMFRINELQKKNLCTVEVSLTYNRYRPLLPSTGKNAKPE 184
 181 HPSTPYVEDLAKLVRSFOEINLMDENKARTVATNMNETSRSNHFVTLTLTQKMH 240
 185 HPSTPYVEDLAKLVRSFOEINLMDENKARTVATNMNETSRSNHFVTLTLTQKMH 244
 241 DEETMDTEKVAKISLVLDAGSERATSGATGARLKEGAEINRSLSLTIGRVIALADMS 300
 245 DAETMDTEKVAKISLVLDAGSERATSGATGARLKEGAEINRSLSLTIGRVIALADMS 304
 301 GQOKKQVLPRYDVTITLTKSLGNSMTAMIAISPADINFEETLSTRVADSARKIK 360
 305 GQOKKQVLPRYDVTITLTKSLGNSMTAMIAISPADINFEETLSTRVADSARKIK 364
 361 NHAIVNEDNARMIRELKEELAQRSKQSSGGG---GGAGGS-----GGPYEESYPPD 412
 365 NHAIVNEDNARMIRELKEELAQRSKQSSGGG---GGAGGS-----GGPYEESYPPD 420
 413 TPLEKQIVSIQOPDATVKKMSKAEIYEQUNOSEKLYRDINQWTEKTLAKTEEIKHREAA 472
 421 TPLEKQIVSIQOPDATVKKMSKAEIYEQUNOSEKLYRDINQWTEKTLAKTEEIKHREAA 480
 473 LBEELGISIFKGVGPRHNSKEMPHLVNLSDDPLLAELVYNIRPGQRRVGNVADOTAER 532
 481 LBEELGISIFKGVGPRHNSKEMPHLVNLSDDPLLAELVYNIRPGQRRVGNVADOTAER 540
 533 LNSGKILKECHTFEENVDNVVTIVPNEKAVMVNGVVIDPTRLRSRGYIILGDFHFRN 592
 541 LNSGKILKECHTFEENVDNVVTIVPNEKAVMVNGVVIDPTRLRSRGYIILGDFHFRN 600
 593 HPEEARAEQEOSLLRHVSNTSOLGSPABGRDRTLKASGADGSRSDSPLPHPRGKD 652
 601 HPEEARAEQEOSLLRHVSNTSOLGSPABGRDRTLKASGADGSRSDSPLPHPRGKD 656
 653 SDMFARREAAAGAILGLDKISHLTDELDALFDVYQKRAVARGIVEDNEDSDGSSFP 712
 657 SDMFARREAAAGAILGLDKISHLTDELDALFDVYQKRAVARGIVEDNEDSDGSSFP 712

QY 713 VDKYWSNGTIDNLSLDTAITMPTPRSDDDGALFEDGKSKQDASNVDEELRQOAO 772
 DB 644 LNNALSSQO-----GVENHSEKAR 664
 QY 773 MEALAKTAKEEF 784
 DB 665 MEALAKTAKEEF 676

RESULT 10
 ID Q4P0W2_USTMA PRELIMINARY, PRT, 1676 AA.
 AC Q4P0W2;
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Hypothetical protein.
 GN ORFNames=DM06251.1;
 OS Ustilago maydis 521.
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 NC NCBI_TaxID=237631;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=521;
 RA Birren B.W., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-Zahra M., Allen T., Allen T., An P., Anderson M., Anderson S.,
 RA Arochchi H.M., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
 RA Bayul T., Bilehseyn B., Bloom T., Biye J., Boguslavskiy L.,
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 RA Engels R., Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J.E., Gealrin G., Gearte S.,
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 RA Lindblad-Toh K., Liu X., Lokysang T., Lokysang Y., Lucien O.,
 RA Lui A., Ma L.-J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marbella R., Maru K., Matthews C., Mauceli E.,
 RA McArthur M., McDonough S., McChae T., Meldrum J., Meneus L.,
 RA Mestrov J., Mhalale A., Milnova T., Mikelsen T., Mlenga V., Moru K.,
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 RA Purrell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
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 RA Rutman M., Schnapbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan T., Sherpa N., Shi J., Smirnov S., Smith C., Sougnuez C.,
 RA Spencer B., Stalker J., Stange-Thomann N., Stavropoulos S.,
 RA Stelson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoulitsang Y., Topham K.,
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V.S., Vanson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wandi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Zander E.S.

RT "The genome sequence of *Ustilago maydis*."
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

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 CC EMBL, AACP01000237; EAK87131.1; -; Genomic DNA.


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DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; F:microtubule-based movement; IEA.
DR InterPro: IPR000253; FHA.
DR InterPro: IPR001752; kinesin_motor.
DR InterPro: IPR001849; PH.
DR Pfam: PF00498; FHA; 1.
DR Pfam: PF00225; Kinesin; 1.
DR Pfam: PF00169; PH; 1.
DR PRINTS: PRO0380; KINESINHEAVY.
DR SMART: SM00129; KISC; 1.
DR SMART: SM00233; PH; 1.
DR PROSITE: PS50006; FHA DOMAIN; 1.
DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE: PS50067; KINESIN MOTOR DOMAIN2; 1.
DR PROSITE: PS50003; PH_DOMAIN; 1.
DR Hypothetical protein.
KW SEQUENCE 1676 AA; 184606 MW; A44A5CD7B2EA99AE CRC64;

Query Match      48.6%; Score 1957.5; DB 2; Length 1676;
Best Local Similarity 51.8%; Pred. No. 4.9e-91;
Matches 426; Conservative 111; Mismatches 194; Indels 91; Gaps 19;

QY 1 MSGGNIKVVVRVPFNAREIDRGACIVR-MEGNOTILTPPGAEKARKSGKTIIDGP 59
DB 1 MDSGNIKVVVRCPMNSRERNRGASNLIEFVDQHLLISPNRPAOTK--ENSKATKKKS 58
QY KAFAPFRSTWSFPMKAPNARQEDLFQDLGVPLLDNAFQYNNCTAYAGQTSGSGKSYSMM 119
DB 60 KAFAPFRSTWSFPMKAPNARQEDLFQDLGVPLLDNAFQYNNCTAYAGQTSGSGKSYSMM 119
QY MPSPSPRAY-----DEHTEODDLFOYIGVELLOHAFNGFNTCVFAYGQTSGSGKSHSV 111
DB 59 MPSPSPRAY-----DEHTEODDLFOYIGVELLOHAFNGFNTCVFAYGQTSGSGKSHSV 111
QY 120 GYKGEHGVPRICQDMFRINE-LQDKKNLTCTVEVSYLEINERVRDLNPSKGNLKY 178
DB 112 GYAQAAGIIPLCARLFEDINQKTADPNLKISVEVSYLEINERVRDLNPNKGNLKY 171
QY 179 REHPSTGYVEDLAKLVRSFOEINLMDGNKARTVAATNNNETSSRSNAVFTLTQK 238
DB 172 REHPSLGPIVEDLSKLVVASYPDIMLMDGNKARTVAATNNNETSSRSNAVFTLTQK 231
QY 239 WHDEFKMTDEKAKISLYDLAGEPATSTGATGARLKKEGAENRSLSTGRVIAALADM 298
DB 232 RPDVQTKLEAEKYSRISMVDLAGSEFANSTGATGARLKKEGANINRSLTTLGKVIALLAIA 291
QY 299 SS-----GKOKK-----NQLVPRDSVLTWLLKDSLGSMSMTAMTAALSPADINEETL 347
DB 292 SSABVEPVKAKKPKTASLDSFVPRDSVLTWLLKDSLGSMSMTAMTAALSPAD--YEETL 349
QY 348 STLRYADSAKRINKHVVNEDPNARMIRLKEELAQLRKSLSSGGGGGAGSGGPPVEE 407
DB 350 STLRYADQAKKIKNKAVNEDPNAKIRLKELELLRTRV---SGGGGAGD-----SS 400
QY 408 STPPTPLEKQIVSIQOPDATVKKMSKAEIVELQNLSEKLYRDLNLTWEKLAKEEIHK 467
DB 401 NMDPSIPDPKQVRYQTGTGEIKTVTKAEIQEQLSEKIMSLNSMSEWELKTKTQEIQK 460
QY 468 EREAALEELGISTEKGFGVRPHYSKEMPHLVNLSDDLLAECLVYNNKPGQTRKGNVNOT 527
DB 461 EBEKALEELGISTVDKNVGHVTPKPLPHLVNLEDDLMSECLLYQIKPGHTLVGNLDSGP 520
QY 528 QAEIRLNGSKILKEHCTFENVDNVVTIIVPEKAAVVNVNGVRI--DKPTRLRSGYRIILGD 585
DB 521 DVHILKSGRIKLNKCMFHQDGLVYVTAMPDSMTVNGKRLAPDPKRLRSRYRIILGD 580
QY 586 FRIIFRNPEEAPAEFQESLLRHSVTNSQLSPAPGRDRTLKSGASDADG--SRSD 642
DB 581 FVAFRNHEEAPAEKADR-----VRSTLALSTGEAHNETL-----IDGDLPSLRDP 626
QY 643 SPLPHRGSDSWFYAREAAAIL-GLDQKISHLDDDELDAFDVQKARA-----693
DB 627 SP-----ASGDVMTTAKRYTAKLNGVNVNEDNLEDELEKLFEDIISRAKSKSGSVL 682
QY 694 ----VARGLVEDNEDSDSSFPVRDKVNSNGTIDNFSILDATITMGTPRASDDGDALFF 749

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DB 683 GRPESPASLFDNDA-----SEASASSVIRYSHGALTDPTSID-----PWSQAGSEKWSRFS 734
QY 750 GDKKSQOD-----ASNDVEELRQOQAOMERAL 777
DB 735 AGPIKENAYTGAGASPALVAASHRETESLRAKVEYEERKL 776

RESULT 11
ID Q8TG36_USTMA PRELIMINARY; PRT; 1676 AA.
AC Q8TG36;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE kinesin.
GN Name=kln3;
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=5270;
RN [1]
RP NCLEOTIDE SEQUENCE.
RX MEDLINE=22060494; PubMed=12065408; DOI=10.1093/emboj/cdf296;
RA Medlich-Solander R., Straube A., Friedrich M.W., Steinberg G.;
RT "A balance of Kif1a-like kinesin and dynein organizes early endosomes
in the fungus Ustilago maydis."
RL EMBO J. 21:2946-2957(2002).
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DR EMBL: AF840446; AL87137.1; -; Genomic_DNA.
DR HSP: P31713; I16T.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; F:microtubule-based movement; IEA.
DR InterPro: IPR000253; FHA.
DR InterPro: IPR001752; kinesin_motor.
DR InterPro: IPR001849; PH.
DR InterPro: IPR011993; PH_type.
DR Pfam: PF00498; FHA; 1.
DR Pfam: PF00225; Kinesin; 1.
DR Pfam: PF00169; PH; 1.
DR PRINTS: PRO0380; KINESINHEAVY.
DR SMART: SM00129; KISC; 1.
DR SMART: SM00233; PH; 1.
DR PROSITE: PS50006; FHA DOMAIN; 1.
DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE: PS50067; KINESIN MOTOR DOMAIN2; 1.
DR PROSITE: PS50003; PH_DOMAIN; 1.
SQ SEQUENCE 1676 AA; 184606 MW; A44A5CD7B2EA99AE CRC64;

Query Match      48.6%; Score 1957.5; DB 2; Length 1676;
Best Local Similarity 51.8%; Pred. No. 4.9e-91;
Matches 426; Conservative 111; Mismatches 194; Indels 91; Gaps 19;

QY 1 MSGGNIKVVVRVPFNAREIDRGACIVR-MEGNOTILTPPGAEKARKSGKTIIDGP 59
DB 1 MDSGNIKVVVRCPMNSRERNRGASNLIEFVDQHLLISPNRPAOTK--ENSKATKKKS 58
QY 60 KAFAPFRSTWSFPMKAPNARQEDLFQDLGVPLLDNAFQYNNCTAYAGQTSGSGKSYSMM 119
DB 59 MPSPSPRAY-----DEHTEODDLFOYIGVELLOHAFNGFNTCVFAYGQTSGSGKSHSV 111
QY 120 GYKGEHGVPRICQDMFRINE-LQDKKNLTCTVEVSYLEINERVRDLNPSKGNLKY 178
DB 112 GYAQAAGIIPLCARLFEDINQKTADPNLKISVEVSYLEINERVRDLNPNKGNLKY 171
QY 179 REHPSTGYVEDLAKLVRSFOEINLMDGNKARTVAATNNNETSSRSNAVFTLTQK 238
DB 172 REHPSLGPIVEDLSKLVVASYPDIMLMDGNKARTVAATNNNETSSRSNAVFTLTQK 231

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239 WHDEETKMDTEKAKISLVDLGSEKATGTGATGARKKEGAENRSLSTLGRVIALADLM 298
 232 RDVDTKLEAEVKSRI SMVDLAGESEANSTGATGARKKAGANINRSLTLGKVIYALALAA 291
 239 SS-----GKOK-----NQLVPRYDSVLTWLLKDSLGSNSMTAMIAISPADINEETL 347
 292 SSAVEPVKAKKPKTASLDSFVPRYDSVLTWLLKOSLGNSXTAMIAISPAD--YEETL 349
 348 STLRYADSKRIKMAVNVNEDPNARIRELKEELNQLREKLOSGSGGCGGAGSGSPVE 407
 350 STLRYADQKKIKMAVNVNEDPNAKIRLEKEELRLTRV---SGGGAGD---ES 400
 408 SYPPDTPLKQIVSIQOPDATYKMSKAEIVQOLNSEKLYVDLNTQTEEKLAKTEEIK 467
 401 NMDPSIIPKQYVRRYQTKGELIKTYKALQOLBQSEKINSLSNBSWEKLTQIOEIK 460
 461 EREKALEELGISVDKGNVGVHTPKLPHLVNINEDPLMECLLYQIKPGHTLVGNLDSGP 520
 468 EREKALEELGISIEKGFVGYPSKEMPHLVNLSDDPLAECLVYNIKPGQTRVGNVNDT 527
 528 QAEILNGSKILKECTFENVNVNVTIVNEKAAVWNVGRI--DKPTLRSGYRIILGD 585
 521 DVHILSGTKILNKICMFDHOGLVTVTAMPDSMTWNGKRLAPDEPKLRSGYRVILGD 580
 586 FIIFFNFHPEEARERQESLRLHSTVNSQLSPAPGRHRTLSKASDADGD---SRSD 642
 561 FIVFFNFHPEEARERQADR-----VRSTLALSTGEAINETL-----IDGDLPESTRD 626
 643 SPLPHFRGKSDWYFARREASAIL-GLDQKISHLTDELDAFDVQKARA----- 693
 627 SP-----ASGDVMTYARREYTMAKLNGQVNFNLDNEEDLEKLFEDISPARSKKSGSVL 682
 694 ----VRGIVENEDSDSGSFYRDKNVNSGNTIDFSLDTAITMGTCTRSDDDGALFF 749
 663 GPRESASLFDUNA---SESASSVIRPYSHGALVTDTSID---FMSQAGSEMGSMRPS 734
 750 GPKKSKD-----ASNVDVELRQOQKQMEAL 777
 735 AGTPIKENAYTGAGASSPALVAASHRETSLSAKKREYEK 776

RESULT 12

055246 CRYNE PRELIMINARY; PRT: 1556 AA.

055246 CRYNE PRELIMINARY; PRT: 1556 AA.
 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 07-FEB-2006, entry version 5.
 DE Hypothetical protein.
 ORFNames=CNB46420;
 OS *Cryptococcus neoformans* var. *neoformans* B-3501A.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomyces; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 NCBI_TaxId=283643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STAIN-B-3501A;
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
 RA Wicks B.L., Fu J., Davis R.W.;
 RT "Cryptococcus neoformans serotype D sequencing";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

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 EMBL; AA01000004; EAL3117.1; -; Genomic DNA.
 DR GO; GO:0005875; C:mitochondrion associated complex; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003777; F:mitochondrial motor activity; IEA.

DR GO:0007018; F:mitochondrion-based movement; IEA.
 DR InterPro: IPR001752; Kinesin_motor.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR01393; PH_type.
 DR Pfam: PF00498; FHA; 1.
 DR Pfam: PF00225; Kinesin; 1.
 DR Pfam: PF00169; PH; 1.
 DR PRINTS: PR00380; KINESINHEAVY.
 DR SMART: SM00129; Kisc; 1.
 DR SMART: SM00233; PH; 1.
 DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1.
 DR PROSITE: PS00067; KINESIN_MOTOR_DOMAIN2; 1.
 DR PROSITE: PS00003; PH_DOMAIN; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 1556 AA; 174143 MW; A91B63EB6130354 CRC64;

Query Match 48.0%; Score 1932.5; DB 2; Length 1556;
 Best Local Similarity 53.0%; Pred. No. 8,4e-90;
 Matches 420; Conservative 99; Mismatches 190; Indels 83; Gaps 14;

4 GGNIVVVRVPRFNAKEIDRGAKEIVRMENQITLTPPGAEEKARKSGKTIIDGPKKAPA 63
 3 GGNIVVVRCPRLNAREIARSGSKELIRNEGSTIIDP---EATGASSKALEKPMIF 59
 64 FDRSYWSP-DKNAFVYARQEDLFODLGVPLLDNAFKGYNNCIFAYGOTGSGKSYSGMGYG 122
 60 FDKSYWASGPKDDPKYASQQTLYEDLDGDLHDHSEFGNTCIFYAGOTGSGKSYSGMGYG 119
 123 KEHGVIPRIQDMFRRIN-ELQDKNLTCTVEVSLEIETNEVRLNLPSTGNLKVNEH 181
 120 AEKGIIPLTTSLEIFRIEARMGSDVNLSTVEVSYLEIETNEKVRDLNPKNGNLRVBEH 179
 182 PSTGPEYEDLAKLVRSFOEINLMDENKARTVATNMNNTSSRSNAVFTL--TLTKM 239
 180 PSLGPEYEDLSLVVENTQMTLMDENKARTVATNMNNTSSRSNAVFTLVLTQKR 239
 240 HDEETKMDTEKAKISLVDLGSEKATGTGATGARKKEGAENRSLSTLGRVIALADMS 299
 240 HDPQTQMGKEKYSKISLVDLGSEKQASTGATGTRLEKGANINKSLTLGKVISALAQG 299
 300 SGQKKQNLVPRDSVLTWLLKDSLGSNSMTAMIAISPADINEETLSTLRYASAKRI 359
 300 ONKRKKEHVPRDSVLTWLLKESLGNSXTAMIAISPAD--YEETLSTLRYADAARKI 357
 360 KMAVNVNEDPNARIRELKEELNQLRSKLSQSGGCGGAGSGGVESYPPDTGLEKQI 419
 358 KTHAVNEDPNAKIRLEKEELRLSRVLSGLSD-----ESSYDSISPEPKQI 407
 420 VSIQOPDATYKMSKAEIVQOLNSEKLYRDNLQTEEKLAKTEEIKEREALAEELGIS 479
 408 VYIIRKEGIRKVTLEHODQLAESEKLMESINLTWEKELQTKQAIHIEREKALAEELGIS 467
 480 IEKGVGPRHSEKEMPHLVNLSDDPLAECLVYNIKPGQTRVGNVNDPQAEIRLNGSKIL 539
 468 IDTNMGVNAIPQNHSLVNLNEDPLMSCLLYQIKPGHTLGAIVED--KAKIKLSGTHIL 526
 540 KEHCTFENVNVNVTIVNEKAAVWNVGRI--DKPTLRSGYRIILGFHIFRNFHPEEA 597
 527 PEHCSFTNDEGVYITLAMPDARTFVNGKRVNPSVYKLLNGFRVILGSHVRRFNDPAV 586
 598 RAERQESLRLHSTVNSQLSPAPGRHRTLSKASDADGDSRSDPLPHFRGKSDWYF 657
 587 RAERKK---LRISSTDENGSLTPG-----LRPDSFSRVDTLEMDWTA 627
 658 ARREASAILGLDQKISHLTDELDAFDVQKAAVNRGLVENEDSDSGSFYRDYK 717
 628 ARREAVD-----IEKLAODDLKLVDILKRTQRRRPSRWDLADFDSHFERSANP 679
 718 MSN-----GTIDNFSIDTAITWGTPRSDDGDALFFDGKSKKODASNVDEEL-RQ 768
 680 LSNPAGREQQTATMTMSNLATFV-----GPDVDAIVIVDEQ 714
 769 QQAQMEALKTA 780

Db 715 SETSAEQALHTS 726

RESULT 13
OSKNGI_CRYNE PRELIMINARY; PRT; 1556 AA.

AC OSKNGI_CRYNE
15-FEB-2005, integrated into UniProtKB/TrEMBL.
07-FEB-2006, entry version 9.

DE Kinesin, putative
GN OrderedLocustNames=CNA06610;
OS Cryptococcus neoformans (Filobasidiella neoformans).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellales; Tremellales; Tremellaceae; Filobasidiella.
NCBI_TaxID=5207;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=UEC21;
RC PubMed=15653466; DOI=10.1126/science.1103773;
RX Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamshayavan J., Miranda M., Anderson J.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grindberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Janson G., Jones S.J.M., Koo H.L., Krzyzanski M.I.,
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Miska R.E.,
RA Mathewson C.A., Mitchell T.G., Petrea M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronsted J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.M.;
RT "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans";
RL Science 307.1321-1324(2005).

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CC EMBL; AE017341; AAM41182.1; -; Genomic DNA.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR001752; kinesin_motor.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH_cyfe.
DR Pfam; PF00498; FHA_1.
DR Pfam; PF00225; kinesin_1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
KM Complete proteome.
SQ SEQUENCE 1556 AA; 174210 MW; D4E65A002B9115B CRC64;

Query Match 47.0%; Score 1895; DB 2; Length 1556;
Best Local Similarity 52.2%; Pred. No. 6; 9e-88;
Matches 412; Conservative 97; Mismatches 191; Indels 90; Gaps 13;

QY 4 GGNIVVAVRPNNAREIDRGAKCIYRMENQITLTPPGAEKARKSKTTMDGKAPA 63
DB 3 GGNIVVAVRCPLNAREIRAGSKELIRMGSSQITLDPF---EATGASSKALEKKPMRS 59
QY 64 FDRSYWVF-DKXAPNVARQEDLFODLGVPLLDNAFVGXNCTFAYGQOTSSGSGSYMGVG 122
DB 60 FDKSYWVAGPQKDDPRYASQOTLIEDGADLLDHSFEGFTCTFAFGQOTSSGSGSYMGVG 119
QY 123 KEHGVIPRICQDMFRIN-ELQKDKNLCTVEVSYLEIYNEHVRDLNPSGTGNLKVREH 181

Db 120 AEGKIIPLTSTSELFRIRIARMGSDVNLSTYVEVSYLEIYNEKVRDLNPNKGNLKVREH 179
QY 182 PSTGPVYEDLAKIWNSSFOEINLMDEGNKARTVAATNNMETSRSNAVATLLUTQKMD 241
DB 180 PSUGPYVEDLSRLVENVYQMTLMDEGNKARTVAATNNMETSRSNAVATLLUTQKMD 239
QY 242 EETKMDTEKVAKISLVDLGASERATSGATGATKEGAEINRSISTLGRVIAALADSSG 301
DB 240 PQTQMGKESKISLVDLGASERATSGATGATGATKEGAEINRSISTLGRVIAALADSSG 299
QY 302 KQKQNLVPRDSVLTWLLKDSLGNSMTAMIAISPADINEETLSTLRVYASAKIKN 361
DB 300 KRKEEHVPRDSVLTWLLKESLGNSKTAMIAI-----STLRVYAAKIKT 348
QY 362 HAVNEDPNAKMLRELKEELAQRLKSLQSSGGGGGAGGAGGSGVESPDPDTLEKQIVS 421
DB 349 HAVNEDPNAKMLRELKEELRLSRVLMGSLD-----ESSYPSIPPEKQIVT 398
QY 422 IQOPDAIVKMSKAEIVQOLNOSEKLYRDLOTWEKLAETEEIHKEREALRELGISTE 481
DB 399 YITKEGEIKVTLQDLQDLASEKLMESLNLTEKLOKTAIHIREKALBELGISTD 458
QY 482 KGFVGPYHSKEMPHLVNLSDPLLAECVYNIKPGQTRVGNVNOQTQABIRLNGSKILKE 541
DB 459 TNNVGVHAPQNHSLVNLNEDPLMSECLYQIKPGTTIAGAVED-KAHIKLSTGTHLPE 517
QY 542 HCFEFVNDVNTIYVPEKAAMVNGVRI--DKPTRLRSGRYIILGDFHIFRNPHEPARA 599
DB 518 HCSFTNDEVVITIEAMPDRTFNGKRVPPNSPVKLLNGFRVTLGDSHFVRFNDPAVRA 577
QY 600 EROEQLSHSTVNSQLGSPAPGRHRTLSKSGSDADGSRSPPLPHRGKOSDMFVVR 659
DB 578 ERKK--LRISSTDENGLTPG-----LRPSPSRVDTLEMDTAR 618
QY 660 REAASAILGLDQKISHLTDELDALFDDYQKAAVARGHVEDNEDSSQSPFVRDKYMS 719
DB 619 REAAD-----IEKLADQDDKLVDLTKLRTQRRRESMDLNDPSSHFRSAPLS 670
QY 720 N-----GTDNRSPLDTAITMPTGTPRSDDGDGDLFPDGKSKODASVNDVEEL-RQOQ 770
DB 671 NPMWAGQQTATMTSLSLATPV-----GPDVDVIVYDEGE 705
QY 771 AQMEBALKTA 780
DB 706 TSAEQALHTS 715

RESULT 14
Q4VXC3_HUMAN PRELIMINARY; PRT; 1153 AA.

AC Q4VXC3;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 5.
DE Kinesin family member 1B.
GN Name=KIF1B; ORFNames=RP4-736L20.1-003;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RA Dunn M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

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CC EMBL; AL358013; CA195222.1; -; Genomic DNA.
DR SMR; Q4VXC3; 4-347.
DR GO; GO:0005874; C:microtubule; IEA.

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DR GO; GO:0005875; C:mitochondrion associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:mitochondrion motor activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0007018; F:mitochondrion-based movement; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR01752; kinesin_motor.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00225; kinesin_1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00240; FHA; 1.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS0006; FHA DOMAIN; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS00677; KINESIN MOTOR DOMAIN2; 1.
DR ATP-binding; Microtubule_Motor protein; Nucleotide-binding.
SQ SEQUENCE 1153 AA; 130363 MW; 6F0D846CD283811 CRC64;

Query Match 42.0%; Score 1691; DB 2; Length 1153;
Best Local Similarity 43.6%; Pred. No. 1,2e-77;
Matches 382; Conservative 137; Mismatches 235; Indels 122; Gaps 19;

OY 4 GGNIRVVVRPFPNAREIDRGAKCIVRMEGNOTILTPPGAEEKARKSGKTIMDGPKAPA 63
DB 3 GASVAVAVRVRFPNRSRETSKESKCIIOGNGNSTSIINPKPKR-----APKSPS 51
OY 64 FDRSYWSF-DKNAPIYARQEDLPOLGVPLDLMNAPGYNCCI FAYGOTGSGKSYMMGQ 122
DB 52 FDISYWSHTSPEDPCFASQNRVYNDIGKMLLHAEFGVNCIFAYGOTGAGKSYTMGQ 111
OY 123 KEH--GVIPRICQDMFRINELQDKNLCTVEVSYLEIYNERVRDLNLPSTKGNLYRE 180
DB 112 EESQNGITPOLCEELFEKIND-NCNEBMSYVSVMETICERVADLNPKNKGLRYRE 170
OY 181 HPSTGPYVEDLAKLVRSFOEINLMDGNKARTVAATNMNETSRSRAVFTLLTQKWH 240
DB 171 HPLGPYVEDLSKLAVTSYTDIADMDAGNKARTVAATNMNETSRSRAVFTIVFQKGG 230
OY 241 DEETKMDREKVAKISLYDLAGEBRATSTAGTARLKEGEINRSLSTLGRVLAALDMS 300
DB 221 DNETLSTEEKSKISLYDLAGEBRADSTAKGTRLEGNINKSLTTLLKVSALAEVSK 290
OY 301 GKOKNQLVPRADSVLTWLLKDSLGSNSMTAMIAISPINFEEITSLTRYADSARKIK 360
DB 291 -KKKTDPIFYDSVLTWLLRENLSGNSKTAIVAAISPADINDETSLTRADRAKQIK 349
OY 361 NHAVVNEDPNAMIRELKEELAQLSKQSSGGGGGAGSGGPGVEEYPPDTLEKQ-- 418
DB 350 CNAVINEDPNAKVRELKEEYTRKDLRAQGLGDIITDSGSLT--SSPSSCSLSQVG 407
OY 419 ---IYSIQPDAIVKMSKAETVEQALNOSEKLYRDLNQTWEKLAETBEIHKREALEE 475
DB 408 LTVSTSIQ--ERIMSTPGGEAEIERLKESEKIIAELNETWEKLRTEAIRERELEAE 465
OY 476 LGISTEK--GFVGPYHSEMPHLVNLDDPLAECIVNIKGGQFVGVNVDQTAERL 533
DB 466 MGAVALREDSGTIGVSPKTPPHLVNLNEBPLMSSECLYITIKGTRVGAADARRDITL 525
OY 534 NGSKILKEHCTFENV---DNVVTIVPNEKAAVMNVGRIDKPTRLRSGRYIILGDFHI 588
DB 526 SGAHKEKEHCIPRSEKSNAGEVIATLEPCERSETYVNGKRVSQPVQLRSGNRIIMGKNV 585
OY 589 FRENPEEARAR-----QEOSLRHSVNSQ-----LGGP 619
DB 586 FRENPEQARAREKTPSAETPSEPVDTWTFQAQRELLKQGIIMKMEKRLQEMETLYKK 645
OY 620 AAGRDRITLSKASDADGDSRSDS----- 643
DB 646 EKEEADLLEQORLADSDSDSKRSCSEBSMKLITSREKLPSKQTIYKKGCLPSS 705
OY 644 -----PLPHFR--GKSDWPFYARREASAILGLDQKISHLTD-----DELDALPD 686
DB 706 GKREPIKMYQIPQRRLSKDSKMWITISDLKIQAVKEICYEVA--LNDPFRHSQREIRALAI 764
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OY 687 DVQKARAVRGLVEDNEDSDSSSFVRDKYMSNGTINDFSIDTAITMGTPRSDP---- 742
DB 765 VAKMELCAMYKKDNE-RDSIRAV-ABDWDIVGVGSEKIEDWATKSGSDIVDDLKYN 822
OY 743 -DGDALFFGDKKSKODASNVDEBELRQQAQWEEAL 777
DB 823 IDKLEDILQEVKKQNMKDEELKVLRNKMLKMEKVL 858

RESULT 15
ID QAR9M8 HUMAN PRELIMINARY; PRT; 1797 AA.
OY QAR9M8;
AC QAR9M8;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE kinesin family member 1beta isoform III.
GN Name=KIF1Bbeta;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Munirajan A.K., Nakagawa A.;
RT "Identification of splicing variants of KIF1Bbeta.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AB088212; BA02545.1; --; mRNA.
DR SMR; QAR9M8; 4-353.
DR GO; GO:0005875; C:mitochondrion associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:mitochondrion motor activity; IEA.
DR GO; GO:0007018; F:mitochondrion-based movement; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR001752; kinesin_motor.
DR InterPro; IPR001849; PH.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00225; kinesin_1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00240; FHA; 1.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS0006; FHA DOMAIN; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS00677; KINESIN MOTOR DOMAIN2; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
SQ SEQUENCE 1797 AA; 201951 MW; 370ACFSB0BD6D15 CRC64;

Query Match 41.8%; Score 1683.5; DB 2; Length 1797;
Best Local Similarity 46.4%; Pred. No. 5.3e-77;
Matches 355; Conservative 126; Mismatches 173; Indels 111; Gaps 15;

OY 4 GGNIRVVVRPFPNAREIDRGAKCIVRMEGNOTILTPPGAEEKARKSGKTIMDGPKAPA 63
DB 3 GASVAVAVRVRFPNRSRETSKESKCIIOGNGNSTSIINPKPKR-----APKSPS 51
OY 64 FDRSYWSF-DKNAPIYARQEDLPOLGVPLDLMNAPGYNCCI FAYGOTGSGKSYMMGQ 122
DB 52 FDISYWSHTSPEDPCFASQNRVYNDIGKMLLHAEFGVNCIFAYGOTGAGKSYTMGQ 111
OY 123 KEH--GVIPRICQDMFRINELQDKNLCTVEVSYLEIYNERVRDLNLPSTKGNLYRE 180
DB 112 EESQNGITPOLCEELFEKIND-NCNEBMSYVSVMETICERVADLNPKNKGLRYRE 170
OY 181 HPSTGPYVEDLAKLVRSFOEINLMDGNKARTVAATNMNETSRSRAVFTLLTQKWH 240
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Db      171 HPLGPEVEDLSKLAVTSYTDIADLMDAGNKARTVAATNNNETSSRSHAVFTIVTQKH 230
Qy      241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARKGAEINRSLSLGRVIAALADM-- 298
Db      231 DNEITNLSIEKVSISLVDLAGSERADSTGAKGRLKGANINKSLTTLGKVISALAEVDN 290
Qy      299 ---SSGKOKKNOQVPRYDSVLTWLLKDSLGNMNTAMIAAISPADINFEETLSTLRVADS 355
Db      291 CTSKSKKKKKTDFIPYRDSVLTWLLRENLDGNSRTAMVAALSPADINVDLTSLRYADR 350
Qy      356 AKRIKHAHVNEPDPNARMIRELKEELAQLRSKLQSSGGG-----GGGAGSGG 402
Db      351 AKQIKCNNAVINEGPNKALVELKEEVTRLKDLRAQGLGDIIDIDPLIDDYSGSGSKSM 410
Qy      403 GPVEEYPPPTPLEKQ-----IVSIQOPDAIVKMSKAEIVEQUNQSEKLYRDLNQTWER 457
Db      411 GSLTSS-PSSCSLSQVGLTSVTSIQ--ERIMSTPGGEAEIERLKESEKIIAEINETWEE 467
Qy      458 KLAKEEIHKEBPAALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECIVYNIKP 515
Db      468 KLRKTEAIRMERBLLAEMGVAIREDGTLGVFSPKKTPHLVNLNEDPLMSECLLYIKD 527
Qy      516 GQTRGVNVDOTQAEIRLNGSKILKEHCTPENV-----DNVVTIVPNEKAAVMVNGVRID 570
Db      528 GITRVGOADAEERODIVLSGAHIKEHCIPRSERNSGEVITYLPCERSETVYNGKRVS 587
Qy      571 KPTRLSGVRITIGDPHIFRNHPEERARARQOSLNRHSVTNSQLGSPAPGRHRTLSK 630
Db      588 QPVQLRSGNRIIGKXHVFRFNHPEQARAEREK----- 620
Qy      631 AGSDADGDSRSDPPLPHFRGKSDWDFYARREAAATILGLDQK-----ISHLTD 678
Db      621 -----TPSAETPEEPVDWTPAOKELLEK-QGIDMKQEMEKRLQEMELIYKKEK 667
Qy      679 DELDALFDD-----VQKARAVRGLVEDNEDSDGSSPP 712
Db      668 BEADLLLEQORLDYESKLGALQKQVETRSLAETTEEBEEEBEEVP 712

```

Search completed: September 1, 2006, 14:33:39
 Job time : 269.166 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 5, 2006, 18:01:01 ! Search time 196 Seconds
(without alignments)
832.787 Million cell updates/sec

Title: US-09-235-416-1_COPY_1_357

Perfect score: 1834

Sequence: 1 MSGGNKIKVVRVPNPARE.....PADINFEETLSTLRVADSAK 357

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 60 summaries

Database :

A_Geneseq.8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1834	100.0	784	2	AAV06618
2	1152	62.8	421	4	AAW41820
3	1152	62.8	1699	8	ABM83651
4	1152	62.8	1708	8	ABM83650
5	1152	62.8	1714	8	ABM83648
6	1152	62.8	1721	8	ABM83647
7	1152	62.8	1721	8	ABM83647
8	1152	62.8	1721	8	ABM83647
9	1152	62.8	1721	8	ABM83647
10	1152	62.8	1721	8	ABM83647
11	1152	62.8	1721	8	ABM83647
12	1152	62.8	1721	8	ABM83647
13	1152	62.8	1721	8	ABM83647
14	1152	62.8	1721	8	ABM83647
15	1152	62.8	1721	8	ABM83647
16	1152	62.8	1721	8	ABM83647
17	1152	62.8	1721	8	ABM83647
18	1152	62.8	1721	8	ABM83647
19	1152	62.8	1721	8	ABM83647
20	1152	62.8	1721	8	ABM83647
21	1152	62.8	1721	8	ABM83647
22	1152	62.8	1721	8	ABM83647
23	1152	62.8	1721	8	ABM83647

24	1063	58.0	1805	5	ABP68930	Abp68930 Human pol
25	1028	56.1	1921	4	ABM62962	Abm62962 Drosophila
26	1027.5	56.0	757	4	AAU19558	AAU19558 Human dia
27	1027.5	56.0	757	4	ABP51294	ABP51294 Human MDD
28	1020.5	55.6	762	5	ABG60124	ABG60124 Human DIT
29	1016.5	55.4	1826	7	ADJ69671	Adj69671 Human hea
30	1016.5	55.4	1826	7	ADL83235	Adl83235 Human PRO
31	1012	55.2	1844	8	ADQ97522	Adq97522 Mouse can
32	1010.5	55.1	1507	8	ADQ97525	Adq97525 Human can
33	990.5	54.0	1815	8	ADQ66952	Adq66952 Human pro
34	990.5	54.0	1815	8	ADQ66954	Adq66954 Human pro
35	990.5	54.0	1815	8	ADQ66951	Adq66951 Human pro
36	990.5	54.0	1815	8	ADQ66953	Adq66953 Human pro
37	987	53.8	359	5	ABM879530	Abm879530 Human kin
38	987	53.8	359	5	ABM84482	Abm84482 Human Hsk
39	987	53.8	359	5	ABM82526	Abm82526 Human Hsk
40	987	53.8	944	7	ADM04401	Adm04401 Human pro
41	987	53.8	944	7	AEC87331	Aec87331 Human CDN
42	987	53.8	1317	9	AED07567	Aed07567 Chromosom
43	987	53.8	1392	6	AAE32129	Aae32129 Human CYT
44	987	53.8	1392	7	ADJ94858	Adj94858 Novel NOV
45	987	53.8	1393	8	ADN00357	Adn00357 Novel hum
46	951.5	51.9	1375	5	ABM79531	Abm79531 Human kin
47	951.5	51.9	1375	5	ABM84481	Abm84481 Human Hsk
48	951.5	51.9	1375	5	AAE22525	Aae22525 Novel NOV
49	947	51.6	1394	7	ADJ94856	Adj94856 Novel NOV
50	913.5	49.8	503	3	AAE63180	Aae63180 Human sec
51	911.5	49.7	504	3	AAE63189	Aae63189 Gene 5 hu
52	873	47.6	1174	4	ABM61704	Abm61704 Human KIF
53	835	45.5	366	9	ADV50400	Adv50400 Human KIF
54	835	45.5	376	9	ADV50399	Adv50399 Human KIF
55	834	45.5	354	9	ADV50396	Adv50396 Human KIF
56	834	45.5	378	9	ADV50398	Adv50398 Human KIF
57	834	45.5	388	9	ADV50397	Adv50397 Human KIF
58	834	45.5	1648	6	ADA83756	Ada83756 Human KIA
59	834	45.5	1648	8	ADO15092	Ado15092 Human can
60	834	45.5	1648	8	ADU06498	Adu06498 Novel bro

ALIGNMENTS

RESULT 1	AAV06618	standard; protein; 784 AA.
ID	AAV06618	
XX		
AC	AAV06618	
XX		
DT	26-OCT-1999	(first entry)
XX		
DE	Thermomyces lanuginosus kinesin motor protein TL-gamma.	
XX		
DE	TL-gamma; kinesin; motor protein; microtubule; unc-104; infection;	
KW	neurodegenerative disease; Alzheimer's disease; Parkinson's disease;	
KW	Huntington's disease; amyotrophic lateral sclerosis.	
OS	Thermomyces lanuginosus.	
XX		
PN	WO937659-A1.	
XX		
PD	29-JUL-1999.	
XX		
PF	22-JAN-1999.	99WO-US001355.
XX		
PR	23-JAN-1998;	98US-0072361P.
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Sakowicz R, Goldstein USB;	
XX		
DR	WPI; 1999-493950/41.	
DR	N-PSDB; AAX87656.	
XX		

PT New nucleic acid encoding microtubule motor protein, used for diagnosis
PT of fungal infection and neurodegenerative disease.
XX
PS Claim 5; Page 70-71; 75pp; English.

CC This sequence represents *Thermomyces lanuginosus* Tl-gamma, a novel ATP-
CC dependent, plus end-directed microtubule motor protein that is a member
CC of the unc-104 family and kinesin superfamily. The invention provides Tl-
CC gamma nucleic acids (see AA87656), proteins and antibodies, and methods
CC of screening for Tl-gamma modulators potentially useful for treating
CC hyphal fungal infections and diseases caused by mutated Tl-gamma, e.g.
CC neurodegeneration involving anterograde axonal transport, such as
CC Alzheimer's, Parkinson's or Huntington's diseases or amyotrophic lateral
CC sclerosis. Detection of Tl-gamma allows differentiation between hyphal
CC and non-hyphal fungal infections

XX Sequence 784 AA;

Query Match 100.0%; Score 1834; DB 2; Length 784;
Best Local Similarity 100.0%; Pred. No. 5, 4e-172;
Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGGGNIKVVVRVPFNAREIDRGAKCIYRMESGNOTILTPPGAEEKARKSGKTTMDGPK 60
DB 1 MGGGNIKVVVRVPFNAREIDRGAKCIYRMESGNOTILTPPGAEEKARKSGKTTMDGPK 60
QY 61 AAFDRSYSPDKNAVNARQEDLPDLGVPLLDNAFKGNNCIPAYGOTSGSKSYMMG 120
DB 61 AAFDRSYSPDKNAVNARQEDLPDLGVPLLDNAFKGNNCIPAYGOTSGSKSYMMG 120
QY 121 YKEHGVIPRICODMERRINELQKDKNLCTVEVSYLEIYNERVRLDLPSTKGNLKVE 180
DB 121 YKEHGVIPRICODMERRINELQKDKNLCTVEVSYLEIYNERVRLDLPSTKGNLKVE 180
QY 181 HPGTGPYVEDLAKLVRSFOEINLMDENKARTVAATNMNETSSGSHAVFTLTQKH 240
DB 181 HPGTGPYVEDLAKLVRSFOEINLMDENKARTVAATNMNETSSGSHAVFTLTQKH 240
QY 241 DEETKMDTEKVAKISLVLAGSERATSGATGARLKEGAINEISLTIGRVIAALDMS 300
DB 241 DEETKMDTEKVAKISLVLAGSERATSGATGARLKEGAINEISLTIGRVIAALDMS 300
QY 301 GQOKNQVLVPRDSVLTWLLKDSLGNSMTAMIAISPADINFEETLSTLRVADSAR 357
DB 301 GQOKNQVLVPRDSVLTWLLKDSLGNSMTAMIAISPADINFEETLSTLRVADSAR 357

RESULT 2
ID AAM41820 standard; protein; 421 AA.

XX AAM41820;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6751.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Dermanac RT;

DR WPI, 2001-442253/47.
DR N-PSDB; AAI60976.

PT Novel nucleic acids and polypeptides, useful for treating disorders such
as central nervous system injuries.

XX Example 2; SEQ ID NO 6751; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the
CC encoded polypeptides (AAM38642-AA442213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 421 AA;

Query Match 62.8%; Score 1152; DB 4; Length 421;
Best Local Similarity 62.1%; Pred. No. 8, 8e-105;
Matches 226; Conservative 58; Mismatches 56; Indels 24; Gaps 6;

QY 4 GGNIKVVVRVPFNAREIDRGAKCIYRMESGNOTILTPPGAEEKARKSGKTTMDGPKAFA 63
DB 9 GASVYVAVRVPFNAREIDRGAKCIYRMESGNOTILTPPGAEEKARKSGKTTMDGPKAFA 63
QY 64 FDRSYWSPDKNAP---NYARQEDLPDLGVPLLDNAFPGYNNCIPAYGOTSGSKSYMMG 120
DB 58 FDRSYWSPDKNAP---NYARQEDLPDLGVPLLDNAFPGYNNCIPAYGOTSGSKSYMMG 115

QY 121 YGK--EHGVIPRICODMERRINELQKDKNLCTVEVSYLEIYNERVRLDLPSTKGNLKVE 178
DB 116 YGK--EHGVIPRICODMERRINELQKDKNLCTVEVSYLEIYNERVRLDLPSTKGNLKVE 174

QY 179 REHPTGPYVEDLAKLVRSFOEINLMDENKARTVAATNMNETSSGSHAVFTLTQKH 238
DB 175 REHPTGPYVEDLAKLVRSFOEINLMDENKARTVAATNMNETSSGSHAVFTLTQKH 234

QY 239 WHDETKMDTEKVAKISLVLAGSERATSGATGARLKEGAINEISLTIGRVIAALDMS 298
DB 235 WHDETKMDTEKVAKISLVLAGSERATSGATGARLKEGAINEISLTIGRVIAALDMS 294

QY 299 SSG-----KOKNQVLVPRDSVLTWLLKDSLGNSMTAMIAISPADINFEETLSTLRV 353
DB 295 SSG-----KOKNQVLVPRDSVLTWLLKDSLGNSMTAMIAISPADINFEETLSTLRV 354

QY 354 DSAK 357
DB 355 DSAK 358

RESULT 3

ID ABM83651 standard; protein; 1699 AA.

ABM83651;

18-NOV-2004 (first entry)

Human diagnostic and therapeutic protein SEQ ID NO:3900.

gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

Homo sapiens.

WO2004023973-A2.

25-MAR-2004.

12-SEP-2003; 2003WO-US028227.

12-SEP-2002; 2002US-0410259P.

12-SEP-2002; 2002US-0410260P.

(INCY-) INCYTE CORP.

Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F, Harthorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV, Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP, Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH, Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL, Lagace RE, Spiro PA, Stewart EA, Wingrove J, Viltz UA, Kitton ES, Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D, Patry S, Shi X, Suarez CU;

WPI; 2004-329368/30.

N-P-SDB; ACN42303.

New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

Claim 27; Page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 272 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorders, endocrine disorders, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dthp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence data represents a dthp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm

Sequence 1699 AA;

Query Match

Best Local Similarity 62.8%; Score 1152; DB 8; Length 1699;

Matches 226; Conservative 58; Mismatches 56; Indels 24; Gaps 6;

4 GGNIKVAVRPPNNAEIDRGAKIVRMGNQITLPPPEAEKARKSGKTTIDGPKARA 63

3 GASVKAIVAVRPPNNAEIDRGAKIVRMGNQITLPPPEAEKARKSGKTTIDGPKARA 63

64 FPRSVSPDKNAP---NYARQEDLPQDLGVPLLDNMFKYNINCFAYGQTGSKSYVMWG 120

DB

52 FDYSYMS--HTSPEDINTYASQKQVARDISEBMLQHPFEGYNYCIFAYGQTGACKSTMMG 109

121 YGR--EHGVIPIRQDMPFRINELQKXNLCTVEVSYLEIYNERVDDLNPSTKGNLKV 178

110 KQKQDQGGIIPQCEDLDFSRINDTND--NMSYSEVSYMEICERVRLDLPNGKNLKV 168

179 REHPSTGPIVEDLAKLVVRSFOEIEENLMBGNKARVVAATNNMETSSRSRAVPTLLTQK 238

169 REHPLLGPYVEDLSKLAVTSYNDIIDLMDSGNKARTVAATNNMETSSRSRAVPTLLTQK 228

239 WHDEETKMDTEKVAKISLVDLAGSEBRTSGATGARLKEGAEINRSISTLGRVIAALADW 298

229 RHDATNITTEKYSKISLVDLAGSEBRTSGATGARLKEGAEINRSISTLGRVIAALADW 288

299 SSG-----KQKXNLVPRDVSULTWLLKDSLGNSTMTAMIISPADINEFTLTLRYA 353

289 DSGPNKMKKKKKTDFPYRDSVLTWLTRENLGNSRTAAVVAALSPADINDEFTLTLRYA 348

354 DSAK 357

349 DRAX 352

DB

RESULT 4

ID ABM83650

ABM83650 standard; protein; 1708 AA.

ABM83650;

18-NOV-2004 (first entry)

Human diagnostic and therapeutic protein SEQ ID NO:3899.

gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

Homo sapiens.

WO2004023973-A2.

25-MAR-2004.

12-SEP-2003; 2003WO-US028227.

12-SEP-2002; 2002US-0410259P.

12-SEP-2002; 2002US-0410260P.

(INCY-) INCYTE CORP.

Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F, Harthorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV, Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP, Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH, Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL, Lagace RE, Spiro PA, Stewart EA, Wingrove J, Viltz UA, Kitton ES, Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D, Patry S, Shi X, Suarez CU;

WPI; 2004-329368/30.

N-P-SDB; ACN42302.

New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

Claim 27; Page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 272 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders, endocrine
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The d1tpp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a d1tpp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

SQ Sequence 1708 AA;

Query Match	62.8%	Score 1152	DB 8	Length 1708
Best Local Similarity	62.1%	Pred. No. 8.7e-104		
Matches 226	Conservative 58	Mismatches 56	Indels 24	Gaps 6

[illegible]

RESULT 5

ID ABM83648 standard; protein; 1714 AA.

AC ABM83648;

DT 18-NOV-2004 (first entry)

DE	Human diagnostic and therapeutic protein SEQ ID NO:3897.
.....	

gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

OS Homo sapiens.

WO2004023973-A2.

25-MAR-2004.

12-SEP-2003: 2003WO-US028227

XX
PR 12-SEP-2002: 200211S-0410259P

PR 12-SEP-2002; 2002US-0410260P.

PA (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthorne TA, Suchorolski MT, Alhus CM, Patre SC, Elder LV;
PI Money EM, Delegane AM, Panzer SI, Bawille S, Reddy TP;
PI Stevens KA, Blanchard JT, Panzer SB, Wang X, Au AP, Geestlin EH;
PI Petalala CH, Anderson SB, Rioux F, Shen ES, Wu MC, Stueve LA;
PI Legace RE, Spiro PA, Stewart EA, Wingoore J, Vilt DA, Kitton ES;
PI Xu Y, Kwong M, Pollicy JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI Patury S, Shi X, Suarez CJ;

DR WPI; 2004-329368/30.
DR N-PSDB; ACN42300.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

PT in gene mapping.

PS Claim 27; Page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorders, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germ-line gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPD at www.wipd.int/pct/en/sequences/listing.htm

... SQ Sequence 1714 AA;

Query Match	62.8%	Score 1152;	DB 8;	Length 1714;
Best Local Similarity	62.1%	Pred. No. 8.7e-104;		
Matches 226; Conservative	58;	Mismatches 156;	Indels 24;	Gaps 6

```

QY      4 GGNIKVVRVVRFPFNAREIDRGAKCIVMEGNGTILTEPPGAEKEARSGKTINDGPAPFA 63
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      3 GASVKAARVVRFPFNRSRSDSKCIIQWSSGTTTTIVNPKOPET-----PKSFS 51
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      64 PDRSVYSPDKNAP---NYARQEDLFODLGVLLDINAEGYNNCIFAAGOTGSKSYSMG 120
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      52 FDSYVYS--HTSPEDINATASOKQYVRDIEGEMLOHAFEGNVCCI FAFQIGQAGAKSYTMG 109
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      121 YGK--EHGVIPRICODMFRRIELOKDKNULTCTVEVSLEYIYNERVDLLINPSTKGNLKY 178
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      110 KQEKDQGGIIPQCEBDFLSRINDTTND--NMSYSEVSVEYMEYICERVDDLINPKQKNLRY 168
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      179 RHHPSRGPRVEDLALVTVRSFOEITENLMBENKARKTAAANNMETSRSRAVETLTLTOK 238
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      169 RHHPLLPGRVEDLSKLAATVSYNDIQDLMDSGNKARTAAATNMETSSRSRAVETLITOK 228
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      239 WHDEETKMDTEKYAKISLVYDLAGESEATSGATARLKEGAETIRSLSTGRVYIALADW 298
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      229 RHDAEINITTEKXKISLVYDLAGESEADSTAKKTRLEKGANINKSLITIGKYSISALAEW 288
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      299 SSG-----KQKNQDLVPRYDSVLTWMLKDSLGSNSMTAMIAISPADINEETLSTLRYA 353
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      289 DSGPNKNNKKKKKTDEPIPRDSVLTWMLRENLGNSRTAMVAALSPADINDETILSTLRYA 348
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      354 DSAK 357
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      349 DRK 352
      ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

RESULT 6

ID ABM83647 standard; protein; 1721 AA.

XX AB083647;
AC
AT 18-NOV-2004 (first entry)
XX
XX
DE Human diagnostic and therapeutic protein SEQ ID NO:3896.
XX
KM gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hatchmore TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleage AM, Panesar IS, Barville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Perella CB, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vltt UA, Kirtson ES;
PI Lu Y, Kwong M, Policky J, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Paury S, Shi X, Suarez CJ;
XX
XX WPI: 2004-329368/30.
DR N-PSDB; ACN42299.
XX
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.
XX
XX
PS Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorders, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dthp protein or the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
XX
SQ Sequence 1721 AA:

Query Match 62.8%; Score 1152; DB 8; Length 1721;
Best Local Similarity 62.1%; Pred. No. 8-8e-104;
Matches 226; Conservative 58; Mismatches 56; Indels 24; Gaps 6

4 GGNKVVVAVPENNAREIDRQKCIIVRMEGNTIILPPGAEKARKSKGKTIIMDKAKA 63
3 GASVAVARVPENSRREMSRDSKCIQMSGTTTIVNPQPKET-----PKSPS 51
64 FDRSAYSPDKNAP---NYARQEDLFQDDGCPPLLDNAFKYNNCIFYAGTGSGSKSYMMG 120
52 FDSYVMS--HNSPEDINTASQKQVARDICEEMNLQHAFEYINVCIFYAGTGSGSKSTMMG 109
121 YGK--EHGVIPRICQDMFRRIEQLQDKNKLCTVEVSYLIEIYNERVRDLLNSTKGNLKY 178

Db	110	KQKDDGGIIPQCELPESFRINDTND-NMSSVEVSYMEYICERVADLNPKNKKLRY	168
Qy	179	REHPSTGPVYEDLAKLVRSFQEIENLMDGKAKATVAATNMNSTRSSHAFTLLTQK	238
Db	169	REHPLGLPYVEDLSKLATVTSYNDIODLMDSGNKAKTVAATNMNSTRSSHAFTNIPQK	228
Qy	239	WHBEETKMTKAYAKSLVDLAGSRRASTGATGARLKEGAEINRSLSLTGLRYAALAD	289
Db	229	RHAEINITTEKRSKISLVDLAGSRRASTGAKGTRLEKANIKSLITLQKVISALAE	288
Qy	299	SSG-----KQKNQALVPYRDSVLTWLLKDSIGNSMTAMIAISPADINFEETSLRYA	353
Db	289	DSEPNKKKKKKKTDFIPYRDSVLTWLLKKNUGNSRTAMVAALSPADINDETSLRYA	348
Qy	354	DSAK 357	
Db	349	DRAK 352	
RESULT 7			
AA0034	AA0034	standard; protein; 893 AA.	
XX	AA0034		
AC	AA0034		
XX			
DT	22-OCT-2001	(first entry)	
XX			
DE		Human polypeptide SEQ ID NO 3179.	
XX			
KW		Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;	
KW		peripheral nervous system; neuropathy; central nervous system; CNS;	
KW		Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
KW		amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;	
KW		chemokinetic; thrombolytic; drug screening; arthritis; inflammation;	
KW		leukaemia.	
XX			
OS	Homo sapiens.		
XX			
PN	WC00153312-A1.		
XX			
PD	26-JUL-2001.		
XX			
PF	26-DEC-2000; 2000MO-US034263.		
XX			
PR	23-DEC-1999; 99US-00471275.		
PR	21-JAN-2000; 2000US-00488725.		
PR	25-APR-2000; 2000US-00552317.		
PR	20-JUN-2000; 2000US-00598047.		
PR	19-JUL-2000; 2000US-00620312.		
PR	03-AUG-2000; 2000US-00653450.		
PR	14-SEP-2000; 2000US-00662191.		
PR	19-OCT-2000; 2000US-00693036.		
PR	29-NOV-2000; 2000US-00727344.		
XX			
PA	(HYSE-) HYSEQ INC.		
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;		
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QH;		
PI	Zhou F, Goodrich R, Drmanac RT;		
XX			
XX	WPI; 2001-442253/47.		
DR	N-PSDB; AAI59190.		
XX			
PT	Novel nucleic acids and polypeptides, useful for treating disorders such		
PT	as central nervous system injuries.		
PS			
PS	Example 4; SEQ ID NO 3179; 10078bp; English.		
XX			
CC	The invention relates to human nucleic acids (AA157798-AA161369) and the		
CC	encoded polypeptides (AA038642-AA042213) with nootropic,		
CC	immunosuppressant and cyostatic activity. The polynucleotides are useful		
CC	in gene therapy. A composition containing a polypeptide or polynucleotide		

CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC activation/inhibition activity, chemocentric/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 893 AA;

Query Match 62.6%; Score 1149; DB 4; Length 893;

Best Local Similarity 61.8%; Pred. No. 6e-104;

Matches 225; Conservative 59; Mismatches 56; Indels 24; Gaps 6;

QY 4 GGNIRKVVVRPFPNAREIDRGACIVRMENQOTILTPPGAEEKARKSGKTIIMDGPKAPA 63

Db 3 GASVKVAIVRFPNREMSRSDSKCIIQMSGSTTTIVNPKPKET-----PKSPS 51

QY 64 FDRSYWSPDKNAP---NYARQEDLPDGLVPLLDNAFGYNNCIFYAGTSGKSYSMWG 120

Db 52 FDSYWA--HTSPEDINVASOKQVYRDIGEBMLQHAFFEGYNCIFYAGTGAGKSYTMWG 109

QY 121 YGK--EHGVIPRICODMPFRINELQDKNLCTVEVSYLEYNERVRDLINPSTGNLKY 178

Db 110 KQEKDQGGIIPQCEDLFSRINDTND--NMSYSVESVSYMEICYERVRDLINPKKGNLRY 168

QY 179 REHPSTGPYVEDLAKLVRSFOEINLMDGKNKARTVAATNMNETSSRSHAVFTLLTQK 238

Db 169 REHPPLGPYVEDLSKLAIVTSYNDIQLMDGKNKARTVAATNMNETSSRSHAVFTLLTQK 228

QY 239 WHDEETKMDTEKAKSLVLDLAGSERATSGATGAKLKEGAEINRSLSITGRVIALADM 298

Db 229 RHDAETNITTEKYSKISLVLDLAGSERADSTGAKGTRLEKANINKSLITLKGKYSALAEW 288

QY 299 SSG-----KOKKQQLVPRDSVLTWLLKDSLGNMNTAMIAISPADINFEETLSTLRVA 353

Db 289 DSGPNKKKKKTDPIFYRDSVLTWLLRENLGNSKRTAMVAALSPADINDETSTLRVA 348

QY 354 DSAK 357

Db 349 DRAK 352

RESULT 8
ABM83653
ID ABM83653 standard; protein; 1696 AA.

XX AC ABM83653;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pproetin SEQ ID NO:3902.

XX DE gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthorne TA, Suchorolski MT, Albus CM, Plets SJ, Elder LV;
PI Mooney EM, Deleagane AM, Panesar IS, Banyille SC, Reddy TP;
PI Stevens KA, Blanchard JT, Panzer SR, Wang X, Au AP, Gerlein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen ED, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Valt UA, Kilton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patuty S, Shi X, Suarez CJ;

XX MPI: 2004-329368/30.

DR N-PSDB: ACN42305.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

PT in gene mapping.

PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides

XX selected from one of the 2722 sequences defined in the specification. A

CC polynucleotide of the invention may have a use in gene therapy. The human

CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

CC used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders,

CC autoimmune/inflammatory disorder, developmental disorder, endocrine

CC disorder, neurological disorders, gastrointestinal disorders, or

CC infections caused by virus, bacteria, fungi or parasite. The dithp

CC molecules may also be used in genetic mapping, in identifying individuals

CC from minute biological samples, in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline

CC gene therapy. The present sequence represents a dithp protein of the

CC invention. Note: The sequence data for this patent is not represented in

CC the printed specification, but was obtained in electronic format directly

CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 1696 AA;

Query Match 62.3%; Score 1142; DB 8; Length 1696;

Best Local Similarity 61.9%; Pred. No. 8.4e-103;

Matches 224; Conservative 59; Mismatches 57; Indels 22; Gaps 6;

QY 4 GGNIRKVVVRPFPNAREIDRGACIVRMENQOTILTPPGAEEKARKSGKTIIMDGPKAPA 63

Db 3 GASVKVAIVRFPNREMSRSDSKCIIQMSGSTTTIVNPKPKET-----PKSPS 51

QY 64 FDRSYWSPDKNAP---NYARQEDLPDGLVPLLDNAFGYNNCIFYAGTSGKSYSMWG 120

Db 52 FDSYWS--HTSPEDINVASOKQVYRDIGEBMLQHAFFEGYNCIFYAGTGAGKSYTMWG 109

QY 121 YGK--EHGVIPRICODMPFRINELQDKNLCTVEVSYLEYNERVRDLINPSTGNLKY 178

Db 110 KQEKDQGGIIPQCEDLFSRINDTND--NMSYSVESVSYMEICYERVRDLINPKKGNLRY 168

QY 179 REHPSTGPYVEDLAKLVRSFOEINLMDGKNKARTVAATNMNETSSRSHAVFTLLTQK 238

Db 169 REHPPLGPYVEDLSKLAIVTSYNDIQLMDGKNKARTVAATNMNETSSRSHAVFTLLTQK 228

QY 239 WHDEETKMDTEKAKSLVLDLAGSERATSGATGAKLKEGAEINRSLSITGRVIALADM 298

Db 229 RHDAETNITTEKYSKISLVLDLAGSERADSTGAKGTRLEKANINKSLITLKGKYSALAEW 288

QY 299 ---SSGKQKQNLVPRDSVLTWLLKDSLGNMNTAMIAISPADINFEETLSTLRVADS 355

Db 289 XPPQKKKKKTDPIFYRDSVLTWLLRENLGNSKRTAMVAALSPADINDETSTLRVADR 348

QY 356 AK 357

Db 349 AK 350

RESULT 9
ABM83652
ID ABM83652 standard; protein; 1697 AA.

XX	AC	ABM83652;
XX	DT	18-NOV-2004 (first entry)
XX	DE	Human diagnostic and therapeutic pprotein SEQ ID NO:3901.
XX	XX	gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX	OS	Homo sapiens.
XX	PN	WO2004023973-A2.
XX	PD	25-MAR-2004.
XX	XX	12-SEP-2003; 2003WO-US028227.
XX	PR	12-SEP-2002; 2002US-0410259P.
XX	PR	12-SEP-2002; 2002US-0410260P.
XX	PA	(INCY-) INCYTE CORP.
XX	PI	Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
XX	PI	Harshorne TA, Suchorolski MR, Altus CM, Plets SJ, Elder LV;
XX	PI	Mooney EM, Delegeane AM, Panssar IS, Banville SC, Reddy TP;
XX	PI	Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
XX	PI	Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
XX	PI	Laugel RE, Siro PA, Stewart EA, Wingrove J, Vilt UA, Kliron ES;
XX	PI	Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gletsen D;
XX	PI	Patury S, Shi X, Suarez CJ;
XX	DR	WPI: 2004-329368/30.
XX	DR	N-PSDB; ACN42304.
XX	PT	New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX	PT	in diagnosing a condition, disease or disorder associated with human
XX	PT	molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX	PT	in gene mapping.
XX	PS	Claim 27; Page: 190pp; English.
XX	XX	The invention relates to novel diagnostic and therapeutic polynucleotides
XX	XX	selected from one of the 2722 sequences defined in the specification. A
XX	XX	polynucleotide of the invention may have a use in gene therapy. The human
XX	XX	diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
XX	XX	used to diagnose a particular condition, disease or disorder associated
XX	XX	with human molecules, e.g. cell proliferative disorders,
XX	XX	autoimmune/inflammatory disorder, developmental disorder, endocrine
XX	XX	disorder, neurological disorders, gastrointestinal disorders, or
XX	XX	infections caused by virus, bacteria, fungi or parasite. The dthp
XX	XX	molecules may also be used in genetic mapping, in identifying individuals
XX	XX	from minute biological samples, in detecting single nucleotide
XX	XX	polymorphisms, as molecular weight markers, and for somatic or germline
XX	XX	gene therapy. The present sequence represents a dthp protein of the
XX	XX	invention. Note: The sequence data for this patent is not represented in
XX	XX	the printed specification, but was obtained in electronic format directly
XX	XX	from WIPO at www.wipo.int/pct/en/sequences/11sting.htm
XX	XX	Sequence 1697 AA:
XX	XX	Query Match 62.3%; Score 1142; DB 8; Length 1697;
XX	XX	Best Local Similarity 61.9%; Pred. No. 8, 4e-103;
XX	XX	Matches 224; Conservative 59; Mismatches 57; Indels 22; Gaps 6
XX	XX	4 GGNIVVVRVRFPNAREIDRGAKCIYMBGNGOTILTPPGAEEKARKSKGTTMDGPKAA 63
XX	XX	3 GASVCAVRAVRFPNSREMSRDSKCIOWSGSTTTIVNPQPKET-----PKSPS 51
XX	XX	64 FDRSIVSFDKNAF---NYARQEDLDQDGLVPLLDNAFKSYNCIFAYGGTGSGKSYSMWG 120
XX	XX	Db 52 FDISYWS--HSPEDINVASQGVYRDISEMLQAHFEGYVNCIFAYGGTGSGKSYTMWG 109
XX	XX	121 YGK--EHGVIPRI CODMFRRI NELQDKNLCTVEVSYLEIYNERVRDLNDSYKGNLKV 178

Db	110	KOEKDOQGIGITPOLCEDLFSRIIDTND-NMSTSVESVWEIYCERRDLINPKGNLNV	168
Qy	179	REHPSGTGYVEDLAKLVVRSEFOEINLDEGNKARTVAATNNNETSSRSHAVFTLLTOK	238
Db	169	REHPLFGYVEDLSLTAATSVSYNDIOLDMSGNKARTVAATNNNETSSRSHAVFNIIFTOK	228
Qy	239	WHDEFTKMDTEKVAKISLVLDLAGSERATSTGATGARLKEGAEINRSLTLGRVIALADM	298
Db	229	RHDAETNITTEKVSKISLVLDLAGSERADSTGAKGRLKEGANINKSLTLGKVISALEM	288
Qy	229	---SSGCKKKQVLVRRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETSLTRYADS	355
Db	289	XPPOKKKKKKTDFIPYRDSVLTWLTRENLGNSRTMAVALSPADINVEETSLTRYADR	348
Qy	356	AK 357	
Db	349	AK 350	
RESULT 10			
ID	ABM83649	standard; protein; 1709 AA.	
XX	AC	ABM83649;	
XX	DT	18-NOV-2004 (first entry)	
XX	DE	Human diagnostic and therapeutic protein SEQ ID NO:3698.	
XX	KM	gene therapy; human diagnostic and therapeutic polynucleotide; dthp.	
XX	OS	Homo sapiens.	
XX	PN	MO2004023973-A2.	
XX	PD	25-MAR-2004.	
XX	PF	12-SEP-2003; 2003WO-US028227.	
XX	PR	12-SEP-2002; 2002US-0410259P.	
XX	PA	12-SEP-2002; 2002US-0410260P.	
XX	PA	(INCY-) INCYTE CORP.	
PI	PI	Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;	
PI	PI	Hatheshorne TA, Suchorolski MT, Altus CM, Pilts SJ, Elder LV;	
PI	PI	Mooney BM, Delegeane AM, Panesar JS, Camille SC, Reddy TP;	
PI	PI	Stevens KM, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;	
PI	PI	Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LJ;	
PI	PI	Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kilton ES;	
PI	PI	Xu Y, Kwong M, Policky UJ, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;	
PI	PI	Pacury S, Shi X, Suarez CU;	
DR	DR	WI; 2004-329368/30.	
XX	DR	N-PSDB; ACN42301.	
XX	PT	New diagnostic and therapeutic polynucleotides and polypeptides, useful	
XX	PT	in diagnosing a condition, disease or disorder associated with human	
XX	PT	molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or	
XX	PT	in gene mapping.	
XX	PS	Claim 27; Page; 190pp; English.	
XX	CC	The invention relates to novel diagnostic and therapeutic polynucleotides	
XX	CC	selected from one of the 2722 sequences defined in the specification. A	
XX	CC	polynucleotide of the invention may have a use in gene therapy. The human	
XX	CC	diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be	
XX	CC	used to diagnose a particular condition, disease or disorder associated	
XX	CC	with human molecules, e.g. cell proliferative disorders,	
XX	CC	autoimmune/inflammatory disorder, developmental disorder, endocrine	
XX	CC	disorder, neurological disorders, gastrointestinal disorders, or	
XX	CC	infections caused by virus, bacteria, fungi or parasite. The dthp	

CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

SQ Sequence 1709 AA:

Query Match 62.3%; Score 1142; DB 8; Length 1709;

Best Local Similarity 61.9%; Pred. No. 8.5e-103;

Matches 224; Conservative 59; Mismatches 57; Indels 22; Gaps 6;

```
4 GGNIKVAVRPPNAREIDRGAKCIVRMEGNQITLPPGAEEKARKSGKTIMDGPKFA 63
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
3 GASVKAARVVRPFNSREMSRDSKCIQMSGSTTTIVNPKQPKET-----PKSFS 51
64 FDRSYWSPDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYMWG 120
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
52 FDIYSYWS--HTSPEDINVASQKQVYRDIGEBMLQHAFFEGYNVCIFAYGQTGAGKSYTMWG 109
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
121 YGK--EHGVIPIRICODMFRRINELQDKKLTCTVEVSYLEIYNERVRLDLNPKGNLKV 178
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
110 KOEKDQOGIIPOLCEDLFSRINDTND--NMSYSVEVSWEIYCERVRDLNPKGNLKV 168
178 RHPSTGPRVEDLAKLVRSFOEINLMDGKARVAATNNMETSRSRSHAVFTLLTQK 238
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
169 RHPPLGPRVEDLSKLAATVSYNDIQDLMDSGNKARTVAATNNMETSRSRSHAVFTLLTQK 228
239 WDEETKMDTEKVAKISLVDLGSEERATSGATGARLKEGAEINRSLSLTGRVIALADM 298
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
229 RHDARTNITTEKYSKISLVDLGSEERADSTGAKGTILKEGANINKSLTLTGKVISALAEH 288
299 ---SSGKQKQKQNLVPRDSVLTWLLKDSLGGNSMTAMIAISPADINFEETLSTLRVADS 355
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
289 XPPONKKKKKTDPIPRDSVLTWLLRENLGGNSRTAMVAALSPADINDETLLSTLRVADR 348
356 AK 357
349 AK 350
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RESULT 11

ID ABM83646 standard; protein; 1722 AA.

ABM83646;

18-NOV-2004 (first entry)

Human diagnostic and therapeutic pprotein SEQ ID NO:3995.

gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

Homo sapiens.

WO2004023973-A2.

25-MAR-2004.

12-SEP-2003; 2003WO-US028227.

12-SEP-2002; 2002US-0410259P.

12-SEP-2002; 2002US-0410260P.

(INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patency S, Shi X, Suarez CJ;
DR WPI: 2004-329368/30.
DR N-PsDB; ACN42298.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

Claim 27; Page: 190pp; English.

CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

SQ Sequence 1722 AA:

Query Match 62.3%; Score 1142; DB 8; Length 1722;

Best Local Similarity 61.9%; Pred. No. 8.6e-103;

Matches 224; Conservative 59; Mismatches 57; Indels 22; Gaps 6;

```
4 GGNIKVAVRPPNAREIDRGAKCIVRMEGNQITLPPGAEEKARKSGKTIMDGPKFA 63
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
3 GASVKAARVVRPFNSREMSRDSKCIQMSGSTTTIVNPKQPKET-----PKSFS 51
64 FDRSYWSPDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGQTGSGKSYMWG 120
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
52 FDIYSYWS--HTSPEDINVASQKQVYRDIGEBMLQHAFFEGYNVCIFAYGQTGAGKSYTMWG 109
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
121 YGK--EHGVIPIRICODMFRRINELQDKKLTCTVEVSYLEIYNERVRLDLNPKGNLKV 178
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
110 KOEKDQOGIIPOLCEDLFSRINDTND--NMSYSVEVSWEIYCERVRDLNPKGNLKV 168
179 RHPSTGPRVEDLAKLVRSFOEINLMDGKARVAATNNMETSRSRSHAVFTLLTQK 238
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
169 RHPPLGPRVEDLSKLAATVSYNDIQDLMDSGNKARTVAATNNMETSRSRSHAVFTLLTQK 228
239 WDEETKMDTEKVAKISLVDLGSEERATSGATGARLKEGAEINRSLSLTGRVIALADM 298
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
229 RHDARTNITTEKYSKISLVDLGSEERADSTGAKGTILKEGANINKSLTLTGKVISALAEH 288
299 ---SSGKQKQKQNLVPRDSVLTWLLKDSLGGNSMTAMIAISPADINFEETLSTLRVADS 355
| : ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : : : : :
289 XPPONKKKKKTDPIPRDSVLTWLLRENLGGNSRTAMVAALSPADINDETLLSTLRVADR 348
356 AK 357
349 AK 350
```

RESULT 12

ABM83671

ID ABM83671 standard; protein; 1199 AA.

ABM83671;

18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic pproteins SEQ ID NO:13920.
DE gene therapy; human diagnostic and therapeutic polynucleotide, ditbp.
KM Homo sapiens.
OS Homo sapiens.
XX MO2004023973-A2.
PN 25-MAR-2004.
XX 12-SEP-2003; 2003WO-US028227.
PF 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410250P.
XX (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorn TA, Suchoroleki MT, Altus CM, Pitter SU, Elder LV;
PI Mooney EM, Deleogene AM, Panesar IS, Barville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rious P, Shen EJ, Wu MC, Stuve LJ;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt VA, Kiron ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patry S, Shi X, Suarez CJ;
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42323.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
PS Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (ditbp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The ditbp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a ditbp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPD at www.wipo.int/pct/en/sequences/listing.htm
XX
XX Sequence 1199 AA;
SQ
Query Match 61.0%; Score 1119; DB 8; Length 1199;
Best Local Similarity 60.8%; Pred. No. 9.1e-101;
Matches 220; Conservative 59; Mismatches 63; Indels 20; Gaps 5;
QY 4 GGNIRKVVVRFPNAREIDRGAKCIVRMEGNQITILPPGAEEKARKSGKTINDGPKAPA 63
DB 3 GASVKAIVAVRPNRNSRSTSKESKCIQMGQNSTSIINPKNPKP-----APKSF 51
QY 64 FDRSYWSF-DKQNPYARQEDLPQDLGVPPLLDNAFKGYNNCIFAYGQSGSKSYMWGK 122
DB 52 FQVSYWSHTSPEDPCFASQRRVYNDIGKEMWLAHAFEGYVNCIFAYGQSGSKSYMWGK 111
QY 123 KEN--GVIPRICODMRARINELQKDKKLTCTVYSYIETINERYRDLINSTGNLKVRE 180
DB 112 EESQAGIIPOLCELEFEKIND-NCNEMSYSVESYVEICERVRDLINPKNGNLKRVRE 170
QY 181 HPGTGPVEDLAKLVVRSFQEIENLMDGKARTVAATNNRSTSSSHAVFTLLTQKMH 240

DB 171 HPLGPEYVEDLSKATATSYDIADMDAGKAKATVAATNNRSTSSSHAVFTLVFOKCH 230
QY 241 DEETKMDTEKVAKISLVDLGASERATSTGATGARLKEGAEINSLTGKVIATLADM-- 298
DB 231 DNETNLSTKESKISLVDLGASERADSTGAKGTRLEKGANINSLTLTGKVISALAEVDN 290
QY 299 ---SSGKOKKNOQVPRDSVLTWLLKDSIGGNMTMIAISPADINFEETSLTRVADS 355
DB 291 CTSKSKKKKKTDFIPYRDSVLTWLLRENLGNSRTAMVAPSPADINVDLSTLRVADR 350
QY 356 AK 357
DB 351 AK 352
RESULT 13
AAB36227
ID AAB36227 standard; protein; 1816 AA.
XX
AC AAB36227;
DT 19-FEB-2001 (first entry)
XX
DE Human kinesin-like protein HKLP SEQ ID NO: 4.
XX
KM Human kinesin-like protein, HKLP; KIF1; cell division; cancer;
KW intracellular transport; neurological disorder; infertility;
KM diallelic marker; spontaneous abortion; neonatal chromosome disorder;
XX aneuploidy.
XX
OS Homo sapiens.
XX
XX MO2000063375-A1.
PN 26-OCT-2000.
PD
XX
PF 20-APR-2000; 2000WO-1B000562.
XX
PR 20-APR-1999; 99US-0130217P.
XX
PA (GENSET) GENSET.
XX
PI Bouguetel L, Dufaure-Gare I, Grel P;
XX WPI; 2000-665242/64.
DR N-PSDB; AAC66550.
XX
XX An isolated or purified human kinesin-like protein (HKLP) encoding
PT polynucleotide used to detect HKLP polynucleotides in a sample comprises
PT a contiguous span of at least 12 nucleotides.
XX
XX Claim 46; Page 189-192; 199pp; English.
XX
XX The present invention describes the coding and protein sequences of the
CC human kinesin-like protein HKLP. It is thought that the protein could be
CC involved in neurological disorders, infertility, spontaneous abortion,
CC neonatal chromosome disorders, aneuploidy and cancers. This is due to its
CC function in the movement of microtubules. The protein shows homology to
CC the murine KIF1A and KIF1B proteins. The sequences disclosed in the
CC invention can be used in the isolation of similar human proteins and in
CC vector production. In addition, the diallelic markers shown can be used
CC in disease diagnosis and population studies
XX
XX Sequence 1816 AA;
SQ
Query Match 61.0%; Score 1119; DB 3; Length 1816;
Best Local Similarity 60.8%; Pred. No. 1.8e-100;
Matches 220; Conservative 59; Mismatches 63; Indels 20; Gaps 5;
QY 4 GGNIRKVVVRFPNAREIDRGAKCIVRMEGNQITILPPGAEEKARKSGKTINDGPKAPA 63
DB 3 GASVKAIVAVRPNRNSRSTSKESKCIQMGQNSTSIINPKNPKP-----APKSF 51

Oy			FDRSWSF-DKNAFYARQEDLFDQLGVPLLLNAPFGYNNCTFAVGTGSSGSYSMMGYG	122
Dd			64 :	
Oy			52 FDSYSTSHSTSPEDPCFASGNRYNDIGKEMLLHAFEGIVNCIFAYQTAGXSYTMWGXQ	111
Dd			123 KEH--GVTPRICODMPRRINELQDKKNLTCTVEVSYLEIYNERRDLNPSTGNLKVRB	180
Oy			112 EESQGIIIPOLCEBELFEKIND-NCNBEMSYSVEVSWMEIYCERVLRLPKNKGNI.RVE	170
Dd			171 HPLLGPYYVEDLSKLAVTSTYTDDIADMDANKARTVAATMNNERSRSHAFTITVFQKH	230
Oy			241 DEETKMDEKYAKISLVLDAGESERTSGTAGARLKEGAENRSJSLTLGRVLAALD.--	298
Dd			231 DNETMLSTEKVSKISLVLDLAGSERADSTGAKGTRLEKANINKSLITLGLVISALEVDN	290
Oy			299 --SSGKKQNQLVPYRDSVT.LTWLLKDSLGGNSMTAMIAAISPADINFEEETLSTRADS	355
Dd			291 CTSMSKKKKKTDFIRYRDSVL.TWLRLRENLGNSRTAMVALSPADLNVDETLSTLYADR	350
Oy			356 AK 357	
Dd			351 AK 352	
RESULT 14				
ID	ABB07867	standard; protein; 1823 AA.		
AC	ABB07867;			
DT	03-JUL-2002	(first entry)		
XX				
DE		Human kinesin-associated protein having motor domain.		
KW		Human; kinesin-associated protein; motor domain; cytoslatic; KIF1B-beta;		
KM		neuroblastoma.		
OS	Homo sapiens.			
PN	WO200226965-A1.			
PD	04-APR-2002.			
PF	01-OCT-2001; 2001WO-JP008635.			
PR	29-SEP-2000; 2000JP-00300247.			
PA	(HISM) HISAMITSU PHARM CO LTD.			
PA	(CHIB-) CHIBA PREFECTURE.			
PI	Nakagawara A;			
WI	WP1; 2002-340013/37.			
DR	N-PSDBI; ABL40908.			
PT		Gene encoding human kinesin-associated protein with motor domain, useful		
PS		for diagnosis and treatment of neuroblastoma.		
XX		Claim 2; Page 40-48; 57pp; Japanese.		
CC		The invention provides a human kinesin-aassociated gene encoding a protein		
CC		having a motor domain and another protein encoded by the human kinesin-		
CC		aassociated gene having no motor domain. The genes are useful for the		
CC		diagnosis and treatment of human neuroblastoma, and judgement of		
CC		prognosis of this disease. Also provided are probes and primers		
CC		hybridising to part of the KIF1B-beta gene, useful for diagnosing		
CC		neuroblastoma in which the gene sequence is detected in tissue samples.		
CC		The present sequence represents a human kinesin-associated protein having		
CC		the motor domain		
XQ	Sequence 1823 AA;			

Query Match	61.0%	Score 1119	DB 5	Length 1823
Best Local Similarity	60.8%	Pred. No. 1.8e-100		
Matches 220	Conservative 59	Mismatches 63	Indels 20	Gaps 5
QY	4	GNKIKVVRVRFNFNAREIDRGAKCIVMEGNOIILTRPPGAEBKARKSGKTIIMDPKFAFA	63	
DB	3	GASVYKVAVRVRFNFRSRETSKESKCIITQIQGNSTSIINDPNKPE-----APKFS	51	
QY	64	FDRSIYMF-DKMANVYARQEDLPDDLGVPLLDNAFKGNNICIFAYGOTSGSKSYMVG	122	
DB	52	FDYSYMSHTSPEDCEFPASQNRVYNDIGKEMILHAFEGNVCIFFAYGQAGAGSYTMWKO	111	
QY	123	KEH--GVYPRICOPMFRINELQDKNLCTVEFSYLEIYNERVARDLLPSTKGLKYRE	180	
DB	112	EESQAGIILPQICELFEKIND-NCNEMSYSEVSESYMEIYERARDLLPNKNGLRARE	170	
QY	181	HPSTGPYVEDIACLVRSPQEIENLMDGNKARTVAATNNNETSSRSHAVFTLLTQKWH	240	
DB	171	HPLLGPYVEDISKLAVSYTDIADLMAGNKARFVAATNNNETSSRSHAVFTIVFTQKCH	230	
QY	241	DEETKMDTEYAKTSLVDLAGSEBATSGATGARTLKGAETNRSLTGRIYALADW--	298	
DB	231	DNEFNLSITEKSKTSLVDLAGSEBADSTGAAGTRLKGAGANINKSLITLIGKISALAEVDN	290	
QY	299	---SSGKOKNQVLVPRDSVLTWLLKSLGNSMTAMIAAISPADINFEETLSTLRVADS	355	
DB	291	CTSKSKKKKKKTDFLPYRDSVLTWLLRNLGNSMTAAVAALSPADINVEDTLSTLRVADR	350	
QY	356	AK 357		
DB	351	AK 352		

XX	AAVS1328 standard; protein; 1103 AA.
XX	AAVS1328
XX	AC
XX	AAVS1328;
DT	17-APR-2000 (first entry)
XX	
DE	Human KLIMP protein.
XX	
KM	KLIMP; kinesin-like motor protein; cytoskeletal; anticonvulsant; human;
KW	anti-Alzheimer; anti-Parkinsonian; antidyspeptic; anti-ulcerative; canc
KW	immunomodulatory; antiinflammatory; anti-AIDS; antineumatic; treatmen
KX	antichronic; diagnosis; neurological disorder; vesicular transport.
XX	
OS	Homo sapiens.
XX	
PN	US6013454-A.
XX	
PD	11-JAN-2000.
XX	
PF	28-SEP-1998; 98US-00162373.
XX	
PR	28-SEP-1998; 98US-00162373.
XX	
PA	(INCY-) INCYTE PHARM INC.
XX	
P1	Tang YT, Corley NC, Patterson C, Guegler KJ;
XX	
DR	WPI; 2000-126064/11.
DR	N-PSDB; AAZ44744.
XX	
PT	Nucleic acid sequences encoding a human kinesin-like motor protein
PT	(KLIMP) useful for the treatment of diseases associated with
PT	inappropriate KLIMP expression such as cancers, neurological disorders
PT	and disorders of vesicular transport.
XX	
BS	Claim 1; Fig 1A-J; 38pp; English.
XX	

CC This invention describes a novel human kinesin-like motor protein (KLIMP)
CC (I) which has cytoskeletal, anticonvulsant, anti-ulcerative, anti-Alzheimer's, anti-
CC Parkinsonian, antidiabetic, anti-rheumatic, immunomodulatory,
CC antiinflammatory, anti-AIDS, antineurotic and antiarthritic activity.
CC (I) and the protein it encodes may be used in the prevention, treatment
CC and diagnosis of diseases associated with inappropriate KLIMP expression
CC such as cancers, neurological disorders and disorders of vesicular
CC transport. For example, (I) (and vectors containing (I) (iv) and the
CC KLIMP polypeptide may be used to treat disorders associated with
CC decreased KLIMP expression such as cancers (e.g. lymphoma, melanoma and
CC cancers of the breast lung and prostate), neurological disorders (e.g.
CC epilepsy, Alzheimer's disease and Parkinson's disease), disorders of
CC vesicular transport (e.g. diabetes mellitus/insipidus, Grave's disease
CC and gastric/duodenal ulcers), and some immune/inflammatory diseases (e.g.
CC acquired immune deficiency syndrome AIDS), rheumatoid arthritis and toxic
CC shock syndrome). This sequence represents the human KLIMP protein
CC described in the method of the invention
XX
XX
SQ Sequence 1103 AA;
Query Match 60.9%; Score 1117; DB 3; Length 1103;
Best Local Similarity 61.6%; Pred. No. 1.3e-100;
Matches 220; Conservative 59; Mismatches 62; Indels 16; Gaps 5;
QY 4 GGNIKVAVRPPNAREIDRGAKCIVRMEGNOTILRPPGAERKARKSGKTINDGKAPA 63
DB 3 GASVKVAVRPPNARETSQDAKCVSMQGNSTSIINP-----KQSDAPKASFT 51
QY 64 FDRSYWSPDKNA-PNYARQEDLFQDILGVPLLDNAFGYNNCIFYAQOTSGKSYMMGYG 122
DB 52 FDRSYWSPDKNA-PNYARQEDLFQDILGVPLLDNAFGYNNCIFYAQOTSGKSYMMGYG 111
QY 123 K--EHGVIPRICODMFRINELQKKNLCTCTVEVSYLEYNERVRLDLPSTGKLVRE 180
DB 112 EFGQGGIVPOLCEDLFSRVSENG-SAQLSYSVEVSWEIYCEVRDLNPKSGSLRVE 170
QY 181 HPSGTGYVEDLAKLVVRSFOEINLMDGKARTVAATNMNNTSSSHAVFTLTLOKXH 240
DB 171 HPLGGYVODLSKLAVTSYADLADLMDCGNKARTVAATNMNNTSSSHAVFTLTLOKXH 230
QY 241 DEETKMDTEKVAKISIVDLAGESEATSGATGARLKEGAENRSLTSGRVIAALADMS 300
DB 231 DQLTGDSERKISIVDLAGESEATSGATGARLKEGAENRSLTSGRVIAALADMS 290
QY 301 GKQKKNQVLPYRDSVLTWLLKDSLGNSMTAMIAISPADINEFTLSTLRVADSAK 357
DB 291 -KKRKSDFIPYRDSVLTWLLKDSLGNSMTAMIAISPADINEFTLSTLRVADRTK 346
RESULT 16
AAE04316
ID AAE04316 standard; protein; 1103 AA.
XX
XX
AAE04316;
XX
XX
10-SEP-2001 (first entry)
DE Human kinesin-like motor protein (KLIMP).
XX
XX
XX Human; kinesin-like motor protein; KLIMP; cancer; adenocarcinoma;
KW leukaemia; lymphoma; melanoma; neurological disorder; epilepsy;
KW ischaemic cerebrovascular disease; stroke; Alzheimer's disease;
KW Pick's disease; Huntington's disease; dementia; Parkinson's disease;
KW vesicular transport disorder; cystic fibrosis; diabetes mellitus; AIDS;
XX Acquired Immune Deficiency Syndrome; microbial infection.
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FT 11..377
FT Domain
FT Binding-site 97..104

FT /note="ATP-binding site"
FT Region 242..253
FT /note="Kinesin motor domain signature"
XX
XX US6248594-B1.
XX 19-JUN-2001.
XX
XX 21-DEC-1999; 99US-00467946.
XX
XX 28-SEP-1998; 98US-00162373.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Tang YT, Corley NC, Guegler KJ, Patterson C;
XX MPI; 2001-407322/43.
XX N-PSDB; AAD08139.
XX
XX Nucleic acid sequences encoding a human kinesin-like motor protein
XX (KLIMP) useful for the prevention and treatment of diseases associated
XX with inappropriate KLIMP expression such as cancers and neurological
XX disorders.
XX
XX Claim 1; Fig 1; 37pp; English.
XX
XX The present sequence is human kinesin-like motor protein (KLIMP) from
XX Incyte clone 128181. KLIMP and the corresponding polynucleotide are
XX useful for diagnosis, treatment and prevention of disorders associated
XX with decreased expression of KLIMP e.g. cancers (such as adenocarcinoma,
XX leukaemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in
XX particular, cancers of the adrenal gland), neurological disorders (such
XX as epilepsy, ischaemic cerebrovascular disease, stroke, cerebral
XX neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease,
XX dementia, Parkinson's disease, peripheral nervous system disorders,
XX mental disorders), and disorders of vesicular transport (such as cystic
XX fibrosis, diabetes mellitus, AIDS (Acquired Immune Deficiency Syndrome),
XX viral, bacterial, fungal, helminthic, and protozoal infections)
XX
XX
SQ Sequence 1103 AA;
Query Match 60.9%; Score 1117; DB 4; Length 1103;
Best Local Similarity 61.6%; Pred. No. 1.3e-100;
Matches 220; Conservative 59; Mismatches 62; Indels 16; Gaps 5;
QY 4 GGNIKVAVRPPNAREIDRGAKCIVRMEGNOTILRPPGAERKARKSGKTINDGKAPA 63
DB 3 GASVKVAVRPPNARETSQDAKCVSMQGNSTSIINP-----KQSDAPKASFT 51
QY 64 FDRSYWSPDKNA-PNYARQEDLFQDILGVPLLDNAFGYNNCIFYAQOTSGKSYMMGYG 122
DB 52 FDRSYWSPDKNA-PNYARQEDLFQDILGVPLLDNAFGYNNCIFYAQOTSGKSYMMGYG 111
QY 123 K--EHGVIPRICODMFRINELQKKNLCTCTVEVSYLEYNERVRLDLPSTGKLVRE 180
DB 112 EFGQGGIVPOLCEDLFSRVSENG-SAQLSYSVEVSWEIYCEVRDLNPKSGSLRVE 170
QY 181 HPSGTGYVEDLAKLVVRSFOEINLMDGKARTVAATNMNNTSSSHAVFTLTLOKXH 240
DB 171 HPLGGYVODLSKLAVTSYADLADLMDCGNKARTVAATNMNNTSSSHAVFTLTLOKXH 230
QY 241 DEETKMDTEKVAKISIVDLAGESEATSGATGARLKEGAENRSLTSGRVIAALADMS 300
DB 231 DQLTGDSERKISIVDLAGESEATSGATGARLKEGAENRSLTSGRVIAALADMS 290
QY 301 GKQKKNQVLPYRDSVLTWLLKDSLGNSMTAMIAISPADINEFTLSTLRVADSAK 357
DB 291 -KKRKSDFIPYRDSVLTWLLKDSLGNSMTAMIAISPADINEFTLSTLRVADRTK 346
RESULT 17
ABG72054
ID ABG72054 standard; protein; 1103 AA.

ABG72054;
31-JAN-2003 (first entry)
Human kinesin-like motor protein, KLIMP.
Human; kinesin-like motor protein; KLIMP; kinesin; microtubule motor protein; ATPase; force; directional movement; agonist; antagonist; diagnostic; transgenic; gene therapy; cancer; neurological disorder; Alzheimer's disease; Parkinson's disease; dementia; epilepsy; vesicular transport; cystic fibrosis; hypercholesterolaemia; diabetes mellitus; hypoglycaemia; hypoglycaemia; gastrointestinal disorder; ulcerative colitis; acquired immunodeficiency syndrome; AIDS; allergy; multiple sclerosis; rheumatoid arthritis; infection; human immunodeficiency virus.
Homo sapiens.
US2002127668-A1.
12-SEP-2002.
02-MAY-2001; 2001US-00847874.
28-SEP-1998; 98US-00162373.
21-DEC-1999; 99US-00467946.
(INCY-) INCYTE PHARM INC.
Tang YT, Corley NC, Guejler KJ, Patterson C; WPI; 2003-066902/06.
N-PSDB; ABS57217.
Novel human kinesin-like motor protein, useful in diagnosis, prevention and treatment of cancer, neurological disorders, and disorders associated with vesicular transport.
Claim 1; Fig 1; 41pp; English.
The invention discloses an isolated human kinesin-like motor protein (KLIMP), and the polynucleotide encoding it. Kinesins are microtubule motor proteins which have an activity that includes microtubule stimulated ATPase activity which generates force and directional movement. The KLIMP protein is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound that specifically binds KLIMP or modulates its activity and for preparing a polyclonal or monoclonal antibody by hybridoma technology. The polynucleotide, polypeptide, antibody and compounds are useful for screening a compound for effectiveness in altering expression of a KLIMP, for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the expression of KLIMP, for detecting KLIMP in a sample and for purifying KLIMP. They are also useful for creating knockin humanised animals or transgenic animals to model human diseases and in somatic or germine gene therapy. The diseases or conditions associated with a modulated expression of functional KLIMP are cancer, a neurological disorder (e.g. Alzheimer's disease, Parkinson's disease, dementia, depression, epilepsy and stroke), a disorder of the vesicular transport (e.g. cystic fibrosis, hypercholesterolaemia, diabetes mellitus, hyper- and hypoglycaemia, Grave's disease, goiter, gastrointestinal disorders such as ulcerative colitis, other conditions associated with abnormal vesicle trafficking such as acquired immunodeficiency syndrome (AIDS), allergic reactions, multiple sclerosis, rheumatoid arthritis and viral, bacterial, fungal, helminthic and protozoal infections). The sequence presented is the human KLIMP protein

OY	4	GGNKKVVRVVRPPNAREIDRGAKCTVRRMEGNOTILTPPGAEBAKRSKSTIMDQKARA	63
OY	4	GGNKKVVRVVRPPNAREIDRGAKCTVRRMEGNOTILTPPGAEBAKRSKSTIMDQKARA	122
Db	3	GASVYVAVRVRPPNARETSODAKCVASMOGNTSTIINP-----KQSKDAVKSFT	51
OY	64	FDRSYWSFDKNA-PNYARQEDLFODLGVPLLDNAEFKGYNNCIFAYGQTSQSGKSYMMGYG	122
Db	52	FDYSYWSHTSTBEDPQFASQGVQYVRIDIGEMMLHNAEGNVNCFAYGQTSQSGKSYTMMGRO	111
OY	123	K-EHGVIPRICQDMFRRINELQDKNLTCTVEVSYLEYINERVDLNPSTKGNLKYRE	180
Db	112	EPGQGVIPOLCEDELFGRVSEHQ-SAQSYSEVSEYMEYTCERVADLNPMSKRGSLRYRE	170
OY	181	HPSTGPEYVEDLAKLVVRSFQEIENLMDGKNKRYTAATNMNETSSRSHAVFTLTLOKH	240
Db	171	HPILCPYQDLSKLAVTSYADLADMDGKNKRYTAATNMNETSSRSHAVFTLVFQRCH	230
OY	241	DEETKMDTEKYAKISLVDLAGSERATSGATGARLKEGAENRSJSTLGRVIAALADMS	300
Db	221	DQLTGLDSEKYSKISLVDLAGSERADSSGARGMGLKEGANIKSLTLTGKVISALADMS	290
OY	301	GKQKKNQLVPRRDSVLTWLKDSLCGNSMTAMIALISPADINFEETLSLTRYADSK	357
Db	291	-KKRSKDEIPRDSVLTWLKLENIGNSRTAMIALSPADINYEETLSLTRYADRTK	346
RESULT 18			
ADG63388	ID	ADG63388 standard; protein; 1103 AA.	
XX	AC	ADG63388;	
XX	DT	11-MAR-2004 (first entry)	
XX	DE	Human kinesin-like motor protein, KLIMP.	
XX	KM	Human; kinesin-like motor protein, KLIMP; cancer; neurological disorder;	
KM	KM	Alzheimer's disease; Parkinson's disease;	
KM	KM	disorder of vesicular transport; cystic fibrosis; hypercholesterolaemia;	
KM	KM	diabetes; Grave's disease; Addison's disease; AIDS;	
KM	KM	autoimmune haemolytic anaemia; glomerulonephritis;	
KM	KM	inflammatory bowel disease; rheumatoid arthritis;	
KM	KM	systemic lupus erythematosus; infections; INCYTE 1281811.	
XX	OS	Homo sapiens.	
XX	PN	US2003207318-A1.	
XX	PD	06-NOV-2003.	
XX	PF	09-JUN-2003; 2003US-00458162.	
XX	PR	28-SEP-1998; 98US-00162373.	
PR	PR	21-DEC-1999; 99US-00467946.	
PR	PR	02-MAY-2001; 2001US-00847874.	
XX	PA	(INCYTE) INCYTE CORP.	
XX	PI	Tang YT, Corley NC, Guegler KJ, Patterson C;	
XX	DR	WPI: 2003-901054/82.	
XX	DR	N-PSDB; ADG63389.	
XX	PT	New human kinesin-like motor protein and polynucleotides, useful for	
PT	PT	diagnosing, preventing or treating diseases or conditions associated with	
PT	PT	aberrant protein expression, e.g. cancer, neurological disorders, AIDS or	
XX	XX	diabetes.	
XX	XX	Claim 1; SEQ ID NO 1; 40pp; English.	
XX	XX	The invention relates to a new isolated polypeptide comprising the human	
CC	CC	kinesin-like motor protein (KLIMP) appearing as ADG63388, a naturally-	
CC	CC	occurring amino acid sequence that is at least 90% identical to KLIMP or	
CC	CC	a biologically active or immunogenic fragment of KLIMP. Also included are	

OY	4	GGNKKVVRVVRPPNAREIDRGAKCTVRRMEGNOTILTPPGAEBAKRSKSTIMDQKARA	63
OY	4	GGNKKVVRVVRPPNAREIDRGAKCTVRRMEGNOTILTPPGAEBAKRSKSTIMDQKARA	122
Db	3	GASVYVAVRVRPPNARETSODAKCVASMOGNTSTIINP-----KQSKDAVKSFT	51
OY	64	FDRSYWSFDKNA-PNYARQEDLFODLGVPLLDNAEFKGYNNCIFAYGQTSQSGKSYMMGYG	122
Db	52	FDYSYWSHTSTBEDPQFASQGVQYVRIDIGEMMLHNAEGNVNCFAYGQTSQSGKSYTMMGRO	111
OY	123	K-EHGVIPRICQDMFRRINELQDKNLTCTVEVSYLEYINERVDLNPSTKGNLKYRE	180
Db	112	EPGQGVIPOLCEDELFGRVSEHQ-SAQSYSEVSEYMEYTCERVADLNPMSKRGSLRYRE	170
OY	181	HPSTGPEYVEDLAKLVVRSFQEIENLMDGKNKRYTAATNMNETSSRSHAVFTLTLOKH	240
Db	171	HPILCPYQDLSKLAVTSYADLADMDGKNKRYTAATNMNETSSRSHAVFTLVFQRCH	230
OY	241	DEETKMDTEKYAKISLVDLAGSERATSGATGARLKEGAENRSJSTLGRVIAALADMS	300
Db	221	DQLTGLDSEKYSKISLVDLAGSERADSSGARGMGLKEGANIKSLTLTGKVISALADMS	290
OY	301	GKQKKNQLVPRRDSVLTWLLKDSLCGNSMTAMIALSPADINFEETLSLRARADSK	357
Db	291	-KKRSKDEIPRDRSVLTWLLKENLGNSRTAMIALSPADINYEETLSLRARADRTK	346
RESULT 18			
ADG63388			
ID	ADG63388	standard; protein; 1103 AA.	
XX	AC	ADG63388;	
XX	DT	11-MAR-2004 (first entry)	
XX	DE	Human kinesin-like motor protein, KLIMP.	
XX	KM	Human; kinesin-like motor protein, KLIMP; cancer; neurological disorder;	
KM	Alzheimer's disease; Parkinson's disease;		
KM	disorder of vesicular transport; cystic fibrosis; hypercholesterolaemia;		
KM	diabetes; Grave's disease; Addison's disease; AIDS;		
KM	autoimmune haemolytic anaemia; glomerulonephritis;		
KM	inflammatory bowel disease; rheumatoid arthritis;		
KM	systemic lupus erythematosus; infections; INCYTE 1281811.		
XX	OS	Homo sapiens.	
XX	PN	US2003207318-A1.	
XX	PD	06-NOV-2003.	
XX	PF	09-JUN-2003; 2003US-00458162.	
XX	PR	28-SEP-1998; 98US-00162373.	
PR	21-DEC-1999; 99US-00467946.		
PR	02-MAY-2001; 2001US-00847874.		
XX	PA	(INCYTE) INCYTE CORP.	
XX	PI	Tang YT, Corley NC, Guegler KJ, Patterson C;	
XX	DR	WPI: 2003-901054/82.	
XX	XX	N-PSDB; ADG63389.	
PT	PT	New human kinesin-like motor protein and polynucleotides, useful for	
PT	diagnosing, preventing or treating diseases or conditions associated with		
PT	aberrant protein expression, e.g. cancer, neurological disorders, AIDS or		
XX	XX	diabetes.	
PS	PS	Claim 1; SEQ ID NO 1; 40pp; English.	
CC	CC	The invention relates to a new isolated polypeptide comprising the human	
CC	kinesin-like motor protein (KLIMP) appearing as ADG63388, a naturally-		
CC	occurring amino acid sequence that is at least 90% identical to KLIMP or		
CC	a biologically active or immunogenic fragment of KLIMP. Also included are		

CC an isolated polynucleotide (NA) encoding KLIMP (appearing as ADG63389, a
CC recombinant polynucleotide comprising a promoter sequence operably linked
CC to the KLIMP NA, a cell transformed with the recombinant polynucleotide,
CC a transgenic organism comprising the recombinant polynucleotide, methods
CC of producing or purifying KLIMP, an isolated antibody, which specifically
CC binds to KLIMP, methods of detecting a target polynucleotide or KLIMP in
CC a sample, compositions comprising the polypeptide, an agonist compound,
CC an antagonist compound or an antibody, and an excipient, methods of
CC treating diseases or conditions associated with decreased expression or
CC overexpression of KLIMP, methods of screening for a compound that is
CC effective as an agonist or antagonist of KLIMP (that specifically binds
CC to KLIMP, that modulates the activity of KLIMP, or is effective in
CC altering expression of the target polynucleotide), a method of screening
CC for potential toxicity of a test compound, a diagnostic test for a
CC condition or disease associated with the expression of KLIMP in a
CC biological sample, methods of diagnosing a condition or disease
CC associated with the expression of KLIMP in a subject, a method of
CC generating an expression profile of a sample containing the
CC polynucleotides and an array comprising different nucleotide molecules
CC affixed at distinct physical locations on a solid substrate, where at
CC least one nucleotide molecule comprises a first oligonucleotide or
CC polynucleotide sequence specifically hybridizable with at least 30
CC contiguous nucleotides of the target polynucleotide. The polypeptides and
CC polynucleotides are useful in diagnosing, preventing or treating diseases
CC or conditions associated with the decreased expression or overexpression
CC of KLIMP, such as cancer, neurological disorders (e.g. Alzheimer's
CC disease or Parkinson's disease), disorders of vesicular transport (e.g.
CC cystic fibrosis, hypercholesterolemia, diabetes, Grave's disease or
CC Addison's disease), AIDS, autoimmune haemolytic anaemia,
CC glomerulonephritis, inflammatory bowel disease, rheumatoid arthritis,
CC fungal, helminthic or protozoal). These are also useful in assessing the
CC effects of exogenous compounds on the expression of nucleic acid and
CC amino acid sequences of KLIMP. The KLIMP or its fragments are useful in
CC screening compounds for effectiveness as agonist or antagonist of the
CC polypeptides, or in altering the expression of the target polynucleotide
CC and compounds that specifically bind to or modulate the activity of the
CC polypeptide. The microarray is useful in monitoring or measuring protein-
CC protein interactions, drug-target interactions, and gene expression
CC profiles. The present sequence represents human KLIMP (INCYTE 1281811).

XX Sequence 1103 AA;

Query Match 60.9%; Score 1117; DB 7; Length 1103;

Best Local Similarity 61.6%; Pred. No. 1.3e-100;

Matches 220; Conservative 59; Mismatches 62; Indels 16; Gaps 5;

QY 4 GGNIKVVRVVRPNAREIDRGAKCIYRMENQOTILRPPGAEEKARKSGKTIIMDGPAFA 63
DB 3 GASVKVAVRVRPNAREIDRGAKCIYRMENQOTILRPPGAEEKARKSGKTIIMDGPAFA 63
XX 3 GASVKVAVRVRPNAREIDRGAKCIYRMENQOTILRPPGAEEKARKSGKTIIMDGPAFA 63

QY 64 FDRSYWSFDMKA-PNVARQEDLFODLGVPLLDNAFKGYNNCFIYAGQTSGSKSYMMGYG 122

DB 52 FDRSYWSHSTSTEDPOFASQOQVVRDICEEMILHAPEGYNVICIYAGQTSGSKSYMMGRQ 111

QY 123 K--EHGVIPRICODMRRINELQDKNLTCTVEVSYLEIYNERVRDLNPNSTGNLKYRE 180

DB 112 EPGQOQIVPOLCELDLSRSVENQ-SAGLSYSVEVSVEIYCEYRDLNPKSGSLRVRE 170

QY 181 HPSTGTYVEDLAKLVVRSFOEINLMDGKNKARTVAATNNNETSSRSASHAVFTLTTLTKQKH 240

DB 171 HPLTGPYVVDLSKLAATSYADIADLMDGKNKARTVAATNNNETSSRSASHAVFTLVFTRQCH 230

QY 241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAINEIRSLTGRVIAALADMS 300

DB 231 DQLTGLDSEKYSKISLVDLAGSERADSSGARGMGLKEGANINKSLTLTGKVISALADMS 290

QY 301 GKGKKNQVLVYRVSYSVLTWLLKDSLGNSGSMRTAATSPADINEEFTLSTARYDSAK 357

DB 291 -KRRKSDPIYRDSVLTWLLKENLGNRSRTAMTAALSPADINEEFTLSTARYADRTK 346

RESULT 19

AAE53317
ID AAE53317 standard; protein; 1770 AA.

XX AAE53317;

DT 17-JUN-2003 (first entry)

DE Mouse KIR1Bbeta protein.

KM KIR1Bb protein; gene therapy; molecular motor protein; kinesin; mouse;

KW KIR1Bbeta gene-associated disease; Charcot-Marie-Tooth disease type 2A;

XX muscular; transgenic.

OS Mus musculus.

XX W0200297079-A2.

PF 29-MAY-2002; 2002MO-JP005226.

PR 29-MAY-2001; 2001US-0293513P.

PA (UYTY) UNIV TOKYO.

PI Hirokawa N, Hayashi Y;

DR WPI; 2003-167270/16.

XX N-PSDB; AAD53964.

PT New KIR1Bb polypeptide having motor activity that transports synaptic

PT vesicle precursor, is useful for developing therapeutic or preventive

PT agent for KIR1Bb gene-associated diseases e.g. Charcot-Marie-Tooth

PT disease type 2A.

PS Claim 1; Page 72-78; 44pp; English.

CC The invention relates to KIR1Bb protein which belongs to kinesin

CC superfamily of molecular motor proteins (Kifs). KIR1Bb is useful for

CC screening for a compound binding to it. Composition comprising the

CC selected compound is useful for treating, alleviating, or preventing a

CC KIR1Bbeta gene-associated disease, in particular Charcot-Marie-Tooth

CC disease type 2A. Transgenic non-human vertebrate, are useful for

CC screening for a candidate compound for treating, alleviating, or

CC preventing a KIR1Bbeta gene-associated disease. KIR1Bb DNA is useful for

CC gene therapy and for recombinant production of polypeptides. KIR1Bb

CC antibody is useful for affinity purification of KIR1Bb and for detecting

CC expression of KIR1Bbeta gene at the protein level. The present sequence

CC is mouse KIR1Bbeta protein

XX Sequence 1770 AA;

Query Match 60.7%; Score 1114; DB 6; Length 1770;

Best Local Similarity 61.3%; Pred. No. 5.4e-100;

Matches 219; Conservative 59; Mismatches 63; Indels 16; Gaps 5;

QY 4 GGNIKVVRVVRPNAREIDRGAKCIYRMENQOTILRPPGAEEKARKSGKTIIMDGPAFA 63
DB 3 GASVKVAVRVRPNAREIDRGAKCIYRMENQOTILRPPGAEEKARKSGKTIIMDGPAFA 63
XX 3 GASVKVAVRVRPNAREIDRGAKCIYRMENQOTILRPPGAEEKARKSGKTIIMDGPAFA 63

DB 231 DETNSTETKVSKITSLVDLAGSRADSTGKGRLEGNINNSLTTLIGVTSALAEVSK 290
QY 301 GKQKKNQLVYPRDSVLTWLLKDSLGNSNTAMTAISPADINEFTLSTLRVDSAK 357
DB 291 -KKKKTDFPYRDSVLTWLLRENLGNSRTAMVAALSPADINDEFTLSTLRVADRAK 346
RESULT 20
AD95088
ID AD95088 standard; protein; 1805 AA.
XX
AC AD95088;
XX
DT 06-MAY-2004 (first entry)
XX
DE Novel NOVX protein sequence #158.
XX
KW antidiabetic; anorectic; cardiast; hypotensive; antiarteriosclerotic;
KW anorectic; vitruclide; antibacterial; fungicide; protozoacide; nootropic;
KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
KW antiautistic; antinflammatory; dermatological; antiaetmatica;
KW antilipemic; gene therapy; metabolic disorder; diabetes; obesity;
KW infectious disease; anorexia; cancer; cardiovascular disease;
KW hypertension; atherosclerosis; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; epileps; immune disorder;
KW osteoarthritis; hematopoietic disorder; inflammatory skin disorder;
KW asthma; dyslipidemia; neurogenesis; cell differentiation;
KW cell proliferation; hematopoiesis; wound healing; angiogenesis;
KW chromosome mapping; tissue typing; pharmacogenomic.
XX
OS Homo sapiens.
XX
PN WO2003040325-A2.
XX
PD 15-MAY-2003.
XX
PF 05-NOV-2002; 2002WO-US035464.
XX
PR 05-NOV-2001; 2001US-0338626P.
PR 06-NOV-2001; 2001US-033072P.
PR 09-NOV-2001; 2001US-034823P.
PR 15-NOV-2001; 2001US-0335610P.
PR 16-NOV-2001; 2001US-0338543P.
PR 20-NOV-2001; 2001US-0331630P.
PR 20-NOV-2001; 2001US-0331641P.
PR 21-NOV-2001; 2001US-0332152P.
PR 27-NOV-2001; 2001US-0333461P.
PR 28-NOV-2001; 2001US-0333912P.
PR 28-NOV-2001; 2001US-0334027P.
PR 29-NOV-2001; 2001US-0334300P.
PR 30-NOV-2001; 2001US-0334421P.
PR 30-NOV-2001; 2001US-0334526P.
PR 04-DEC-2001; 2001US-0336576P.
PR 04-DEC-2001; 2001US-033664P.
PR 07-DEC-2001; 2001US-0338314P.
PR 07-DEC-2001; 2001US-0338390P.
PR 10-DEC-2001; 2001US-0339006P.
PR 10-DEC-2001; 2001US-0339008P.
PR 11-DEC-2001; 2001US-0339286P.
PR 01-FEB-2002; 2002US-0353280P.
PR 01-FEB-2002; 2002US-0353388P.
PR 04-FEB-2002; 2002US-0354392P.
PR 04-FEB-2002; 2002US-0354393P.
PR 04-FEB-2002; 2002US-0354409P.
PR 27-FEB-2002; 2002US-035944P.
PR 27-FEB-2002; 2002US-0360148P.
PR 05-MAR-2002; 2002US-0361790P.
PR 05-MAR-2002; 2002US-0361833P.
PR 05-MAR-2002; 2002US-0362230P.
PR 05-MAR-2002; 2002US-0362625P.
PR 13-MAR-2002; 2002US-0364000P.

PR 13-MAR-2002; 2002US-0364181P.
PR 13-MAR-2002; 2002US-0364182P.
PR 13-MAR-2002; 2002US-0364197P.
PR 13-MAR-2002; 2002US-0364227P.
PR 17-MAY-2002; 2002US-0381621P.
PR 28-MAY-2002; 2002US-0383675P.
PR 17-JUL-2002; 2002US-0396703P.
PR 06-AUG-2002; 2002US-0401552P.
PR 07-AUG-2002; 2002US-0401594P.
PR 07-AUG-2002; 2002US-0401787P.
PR 15-AUG-2002; 2002US-0403619P.
PR 20-AUG-2002; 2002US-0404821P.
PR 23-AUG-2002; 2002US-0405368P.
PR 23-AUG-2002; 2002US-0405402P.
PR 23-AUG-2002; 2002US-0405496P.
PR 23-AUG-2002; 2002US-0405631P.
PR 26-AUG-2002; 2002US-0406125P.
PR 04-NOV-2002; 2002US-00287226.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Agee ML, Alsobrook JP, Berghs C, Boldog FL, Burgess CE, Chant JS;
PI Chaudhuri A, Diptipo VA, Edinger SR, Eissen A, Elberman K,
PI Gangoli EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khrantsov NV;
PI Li L, Malvankar UM, Macdougall JR, Mezes PS, Miller CE, Millet I;
PI Ooi CE, Ort T, Padigaru M, Patrajan M, Raestelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Spaderna SK, Spletke KA, Taupier RJ;
PI Vernet CM, Zernusen BD, Zhong M;
XX
DR WPI; 2003-41551/41.
DR N-PSDB; AD95087.
XX
PT New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
PT asthma, or infections.
XX
PS Claim 1, SEQ ID NO 316; 800pp; English.
XX
CC The invention relates to novel isolated polypeptides, mature forms of
CC these, or a sequence that is at least 95 % identical to, or having one or
CC more conservative amino acid substitutions in the polypeptides. The
CC polypeptides, nucleic acid molecules and antibodies are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOVX-associated disorder. The nucleic acid
CC molecules, polypeptides and antibodies are useful for treating,
CC preventing or diagnosing diseases such as metabolic disorders, diabetes,
CC obesity, infectious diseases (viral, bacterial, fungal, helminthic, and
CC protozoal), anorexia, cancer, cardiovascular diseases (hypertension,
CC atherosclerosis), neurodegenerative disorders, Alzheimer's disease,
CC Parkinson's disease, epileps, immune disorders (osteoarthritis),
CC hematopoietic disorders, inflammatory skin disorders, asthma, and various
CC dyslipidemias. The nucleic acids and polypeptides may also be used as
CC targets for the identification of small molecules that modulate or
CC inhibit e.g. neurogenesis, cell differentiation, cell proliferation,
CC hemopoiesis, wound healing and angiogenesis, in gene therapy, in
CC generation of antibodies that bind immunospecifically to NOVX substances
CC for use in therapeutic or diagnostic methods. The nucleic acids are
CC further used as hybridization probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. This sequence
CC corresponds to one of the NOVX polypeptides of the invention.
XX
SO Sequence 1805 AA:
Query Match 60.7%; Score 1112.5; DB 7; Length 1805;
Best Local Similarity 61.5%; Pred. No. 7.9e-100;
Matches 220; Conservative 59; Mismatches 62; Indels 17; Gaps 6;
QY 4 GGNIKVVVRVPFNREIDRGAKCIVRMENQNTILTPPGAEKARKSGKTTMDPKAPA 63
DB 3 GASVKVAARVPFNSRSTSKSKCIIOMGNSTSLNKNPKE-----APKSS 51
QY 64 FDRSYWSP-DKNAPYARQEDLFDLDLGVPLLDNAEKGYNNCTIFAYGQTGSGKSYMMGYG 122

```

Db      52 FDYSYSHTSPEDEPCFASQNRVYNDIGKEMLLHAFEBYNNCFIAYGOTGAGKSTMMGKQ 111
Qy      123 KEH--GVIPRICODMRMRINELQOKNKLCTTVEYSYLEIYNERVRLDLNSTGKMKVRE 180
Db      112 EESQAGIIPOLCELEPEKIND-NCNEMSYSEVSWEIYCERVRDLNPKNGNLRVRE 170
Qy      181 HPSTGPRVEDLAKLVRSFOEINLMDENKARTVAATNNNETSSRSHAVFTTLTQKMH 240
Db      171 HPLGPRVEDLSKLATYSTYDIDLMDAGNKARTVAATNNNETSSRSHAVFTTQKMH 230
Qy      241 DEETKMDTER-VAKISLVDLASERATSTGATGARLKEGAEINRSLSLGRVIALADMS 299
Db      231 DNETNSTEKVSKISLVDLASERADSTGAKGRLEKGANINKSLTTLGKVISALAEVS 230
Qy      300 SGOKKQNLVPRYDSVLTWLLKDSLGNSMTAMIAISPADINFEETLSTLRVADS 357
Db      291 K-KKKKTDFIPYRDSVLTWLLRENLGNSRTAMVAALSPADINVEFTLSTLRVADRAK 347

RESULT 21
ADV50414 ID ADV50414 standard; protein; 365 AA.
ADV50414 AC
ADV50414:
XX      10-MAR-2005 (first entry)
XX      Human KIF1B motor domain.
XX      ATPase modulator; kinesin family 1B; KIF1B; kinesin; cell proliferation;
XX      hyperproliferative disorders; cancer; breast tumor; resection;
XX      cardiovascular disease; autoimmune disease; immune disorder; arthritis;
XX      inflammation; musculoskeletal disease; graft rejection;
XX      inflammatory bowel disease; gastrointestinal disease; cytostatic;
XX      vasotropic; immunosuppressive; antiarthritic; antiinflammatory;
XX      gastrointestinal-gen.
XX
XX      Homo sapiens.
XX      WO2004109290-A2.
XX
XX      16-DEC-2004.
XX
XX      28-MAY-2004; 2004WO-US017234.
XX
XX      30-MAY-2003; 2003US-0474488P.
XX      03-JUN-2003; 2003US-0475873P.
XX      17-MAR-2004; 2004US-0553838P.
XX
XX      (ROSE-) ROSETTA INPHARMATICS LLC.
XX      (MERI) MERCK & CO INC.
XX
XX      Mao M, Linsley PS, Buser CA, Marshall CG, Kim AS;
XX      MPI; 2005-057663/06.
XX
XX      Screening for modulators of target protein e.g., kinesin family 14
XX      protein, by contacting target protein with candidate agent, and
XX      determining whether candidate agent modulates activity of target protein.
XX      Example 7; SEQ ID NO 21; 118pp; English.
XX
XX      The invention relates to a method (M1) of screening for modulators of a
XX      target protein. The method involves contacting the target protein with
XX      candidate agent, and determining whether the candidate agent modulates
XX      activity of target protein, where the target protein comprises a sequence
XX      that has more than 80% amino acid sequence identity to a fully defined
XX      kinesin family 14 (KIF14) protein (SEQ ID No:2) or the KIF14 motor domain
XX      sequence (SEQ ID No:3). Also described are: a method (M2) for modulating
XX      cell proliferation, a method (M3) for treating a subject with a cellular
XX      hyperproliferation disorder, a method (M4) for identifying candidate
XX      subjects for treatment with an inhibitor of the activity of a target

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CC      protein, and a kit for screening for modulators of a target protein. A
CC      cell viability assay, cell morphology assay, cell proliferation assay,
CC      cell cycle distribution assay or apoptosis assay is used for determining
CC      whether the candidate agent modulates the activity of the target protein.
CC      The target protein comprises SEQ ID No:2, SEQ ID No:3, or a fragment of
CC      SEQ ID No:3 having Arpase activity. The modulator is an inhibitor such as
CC      RNA inhibitor, which is a KIF14 RNA inhibitor. The KIF14 RNA inhibitor
CC      comprises sequence such as those disclosed in SEQ ID Nos 8, 9 or 23.
CC      Method (M1) is useful for screening for modulators of a target protein,
CC      particularly for screening modulators of KIF14 or KIF14 motor domain.
CC      Method (M2) is useful for treating a subject with a cellular
CC      hyperproliferation disorder such as cancer, preferably breast cancer.
CC      Method (M3) is useful for treating resection, autoimmune disease,
CC      arthritis, graft rejection or inflammatory bowel disease. This sequence
CC      represents human KIF1B motor domain.
XX
XX      SQ      Sequence 365 AA;
XX
XX      Query Match      60.6%; Score 1111; DB 9; Length 365;
XX      Best Local Similarity 60.7%; Pred. No. 8.2e-101;
XX      Matches 218; Conservative 59; Mismatches 62; Indels 20; Gaps 5;
XX
Qy      4 GGNIKVVRVPRPNAREIDRGAKCIVRMEGNQITLPPGAEERKARKSGKTIIDGPKAF 63
Db      3 GASVKVAVRPRPNRSRSTSKESKCIIOGNGNSTSIINPKNPKR-----ARKSFS 51
Qy      64 FDRSYWSF-DKQAPNARQEDLEFQDLGVPLDANAFKYNNCIFAYQOTSGSKSYMMG 122
Db      52 FDYSYSHTSPEDEPCFASQNRVYNDIGKEMLLHAFEGYNNCFIAYGOTGAGKSTMMGKQ 111
Qy      123 KEH--GVIPRICODMRMRINELQOKNKLCTTVEYSYLEIYNERVRLDLNSTGKMKVRE 180
Db      112 EESQAGIIPOLCELEPEKIND-NCNEMSYSEVSWEIYCERVRDLNPKNGNLRVRE 170
Qy      181 HPSTGPRVEDLAKLVRSFOEINLMDENKARTVAATNNNETSSRSHAVFTTLTQKMH 240
Db      171 HPLGPRVEDLSKLATYSTYDIDLMDAGNKARTVAATNNNETSSRSHAVFTTQKMH 230
Qy      241 DEETKMDTER-VAKISLVDLASERATSTGATGARLKEGAEINRSLSLGRVIALADMS 298
Db      231 DNETNSTEKVSKISLVDLASERADSTGAKGRLEKGANINKSLTTLGKVISALAEVDN 230
Qy      299 ----SSGOKKQNLVPRYDSVLTWLLKDSLGNSMTAMIAISPADINFEETLSTLRVAD 354
Db      291 CTSKSKRKKKTDFIPYRDSVLTWLLRENLGNSRTAMVAALSPADINVEFTLSTLRVAD 349

RESULT 22
ABB63908 ID ABB63908 standard; protein; 1773 AA.
ABB63908:
XX      ABB63908;
XX
XX      26-MAR-2002 (first entry)
XX
XX      Drosophila melanogaster polypeptide SEQ ID NO 18516.
XX
XX      Drosophila; developmental biology; cell signalling; insecticide;
XX      pharmaceutical.
XX
XX      Drosophila melanogaster.
XX
XX      WO200171042-A2.
XX
XX      27-SEP-2001.
XX
XX      23-MAR-2001; 2001WO-US009231.
XX
XX      23-MAR-2000; 2000US-0191637P.
XX      11-JUL-2000; 2000US-00614150.
XX
XX      (PEKE ) PE CORP NV.
XX

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PI Venter JC, Adams M, Li PMD, Myers EW;
 XX WPI: 2001-656860/75.
 DR N-PSDB; ABL08011.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from *Drosophila* and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 18516; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1773 AA;

Query Match 60.3%; Score 1106.5; DB 4; Length 1773;
 Best Local Similarity 62.4%; Pred. No. 3e-99;
 Matches 222; Conservative 52; Mismatches 69; Indels 13; Gaps 4;

QY 6 NIKVVVRVPPFNAREIDRGAKCIVRMENQITLTPPGAEBKARKSGKTI MGPKAFAD 65
 DB 32 SYKVAARVPPFNAREIDRGAKCIVRMENQITLTPPGAEBKARKSGKTI MGPKAFAD 83
 QY 66 RGYWFRDKKAPYARQEDFDLQDGVPLLNAPFGYNNCTFAYGQTSGSGKSMGQKGE 124
 DB 84 YSWSHDHDADPSTQSMYVKDGEEMLOHSPDGIVNCIFAYGQTSGSGKSMGQKGE 143
 QY 125 -HGVIPIRIGQDFRINELQDKNLTCTVEVSLYEIYNRVRDLNPSKGNLKVREHPS 183
 DB 144 QGGIIPMICDKLFTTRIGDTEBD-DLKYSEVSVSMETCYCERVRLNPKKGNIRVHEHL 202
 QY 184 TGPVYEDLAKLVRSFOEINIMDEGNKARVVAATNMNETSSRSHAVFTLLTQKMHDEE 243
 DB 203 LCPVYEDLSKLAVTQDIDHDLIDEGNKARTVAATNMNETSSRSHAVFTLFTQRSHDLM 262
 QY 244 TMDNPEKVAKISLVNDAGSERATSGATGARLKEGAENIRSLTICRVIAALADMSGKO 303
 DB 263 TWLITTEKYSKISLVNDAGSERADSTGAKGRLEKGNINIKSLTTLKVISALAEVASKKK 322
 QY 304 --KKQQLVPRDSVLTWLTMLKDSIGNSMTAMIAISPADINEETLSTRYADSAR 357
 DB 323 NTKKADFIYRDSALTWLIRENIGNSKTMIAISPADINDETSTIRYADRAK 378

RESULT 23
 AAU74840
 ID AAU74840 standard; protein; 1362 AA.

AC AAU74840;

XX 10-APR-2002 (first entry)
 DT Human Hskf13a protein sequence.
 DE
 XX

XX Hskf13a; human; kinesin; microtubule motor protein; cytosolic;
 KW vulnary; antirheumatic; antiarthritic; antigout; antiinflammatory;
 KW vasotrophic; neuroprotective; cytoskeletal; atherosclerosis; cancer;
 KW haematopoietic tumour; tumour metastasis; benign tumour; haemangioma;
 KW acoustic neuroma; wound healing; rheumatoid arthritis; psoriasis;
 KW Behcet's disease; gout; gouty arthritis; angioneuromatosis;
 KW rheumatoid arthritis; diabetic retinopathy; neurological disorder;
 KW vesicular transport disorder.

XX Homo sapiens.
 OS

XX Key location/Qualifiers
 FH 1.352
 FT Domain
 FT /note="Hskf13a motor domain, this sequence is
 FT specifically claimed in claim 8 of the specification"
 FT Misc-difference 540
 FT /label= Unknown
 FT /note= "Encoded by AGN"
 FT Misc-difference 541..563
 FT /label= Xaa
 FT /note= "Amino acid residues 541-563 are all Xaa, and are
 FT all encoded by NNN"
 FT Misc-difference 564
 FT /label= Unknown
 FT /note= "Encoded by NNA"
 FT Misc-difference 747..769
 FT /note= "Amino acid residues 747-769 are all Xaa, and are
 FT all encoded by NNN"
 FT Misc-difference 770
 FT /label= Unknown
 FT /note= "Encoded by NGR"

XX WO200192467-A2.

XX 06-DEC-2001.

XX 26-MAY-2001; 2001WO-US017148.

XX 26-MAY-2000; 2000US-00580928.

XX (CYTO-) CYTOKINETICS INC.

PI Berard C, Freedman R;

XX WPI: 2002-075464/10.

DR N-PSDB; ABR13131.

XX Human microtubule motor protein, Hskf13a, useful for screening
 PT modulators of Hskf13a which are used for modulating cytoskeletal system
 PT in conditions of benign tumors and rheumatoid arthritis.

XX Claim 11; Fig 2; 55pp; English.

XX This invention relates to the nucleic acid and protein sequence of a
 CC novel microtubule motor protein Hskf13a. The protein of the invention
 CC may have cytoskeletal; vulnary; antirheumatic; antiarthritic; antigout;
 CC antiinflammatory; vasotrophic; neuroprotective activities and may act as a
 CC cytoskeletal system modulator. The Hskf13a nucleic acid is useful for
 CC screening for modulators of Hskf13a, such modulators would be useful for
 CC modulating cytoskeletal system for treating conditions such as abnormal
 CC stimulation of endothelial cells (e.g., atherosclerosis), solid and
 CC haematopoietic tumours and tumour metastasis, benign tumours, e.g.,
 CC haemangiomas, acoustic neuromas, etc., abnormal wound healing, rheumatoid
 CC arthritis, Behcet's disease, gout or gouty arthritis, abnormal
 CC angiogenesis accompanying: rheumatoid arthritis, psoriasis, diabetic
 CC retinopathy, etc. The sequences of the invention are useful for the
 CC diagnosis, treatment, or prevention of cancer, neurological and vesicular
 CC transport disorders. Nucleic acids encoding the kinesins are useful for
 CC identifying polymorphic variants, orthologues, alleles and homologues of
 CC Hskf13a. Hskf13a and its homologues are also useful as diagnostic tools
 CC in vitro. The kinesins and in particular their motor domains can be used
 CC for separation of a specific ligand from a heterogeneous mixture in
 CC aqueous solution. The kinesins and in particular their motor domains can
 CC also be used in the field of nanotechnology. The present sequence
 CC represents the human Hskf13a protein sequence of the invention

XX Sequence 1362 AA;

Query Match 58.0%; Score 1063; DB 5; Length 1362;
 Best Local Similarity 60.1%; Pred. No. 4e-95;
 Matches 212; Conservative 62; Mismatches 69; Indels 10; Gaps 5;

QY 7 IKVVVRVPPFNAREIDRGAKCIVRMENQITLTPPGAEBKARKSGKTI MGPKAFAD 66

DB 6 VKAAVAVRPMNRRELNTKCVEMEGNQTVLHPPSNTKQGERK-----PKVFAFDY 59
QY 67 SYWSPDK-NAPNYARQEDLFODLGVPLDPAFKGVNNCIFAYGQTSGSKSYMMGYGKEH 125
DB 60 CFWSMDESNTTKYAGQEVVFKLGGEGILEKAFQGVNACIFAYGQTSGSKSFMMGHAEQL 119
QY 126 GVLPRIQDMFRINLEQDKNLTCTVEVSYLEIYNERVRLDLP-STKGNLKVREHPST 184
DB 120 GLIPRLCALFKRIS-LEQNESQTFKVEVSYMEIYNEKVRDLDPKGRSLKVREHKVL 178
QY 185 GPVEDLAKLVRSFOEINLMDGNKARTVAATNNNETSSRSHAVFTLLTQKMHDEET 244
DB 179 GPYVDLSQLAVTSFEDISLMSSEGNKSRVAATNNBESSRSHAFNIIITQTLVDLOS 238
QY 245 KMDTEKVAKISLVDLGSRATSTGATGARLKEGABINRSLSTLGRVIALADMMSSGKOK 304
DB 239 GNSGEKYSKSVSLVDLAGSERVSKTGAAGERLKEGNSINKSLTTLGLVYISLADQAGK-G 297
QY 305 KQQLVYPRDSVLTWLTLDKSLGNSMTAMTAISPADINFEETLSTLRVADSAR 357
DB 298 KSKFVYPRDSVLTWLTLDKSLGNSQTSMTATISPADNVEETLSTLRVADRAK 350
RESULT 24
ABP68930
ID ABP68930 standard; protein; 1805 AA.
XX
AC ABP68930;
XX
DT 20-JAN-2003 (first entry)
DE Human polypeptide SEQ ID NO 977.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
cell-proliferative disorder; neurodegenerative disease; bacterial;
Parkinson's disease; Alzheimer's disease; autoimmune disease;
multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Auendi V, Zhang J, Zhao QA, Ren F;
Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drihanac RT;
XX
DR MPI; 2002-759812/82.
XX
N-PSDB; AB211147.
XX
PT New polynucleotides comprising sequences assembled from expressed
sequence tags (ESTs), useful for treating cell-proliferative,
neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
or coagulation disorders.
XX
XX Claim 9; SEQ ID NO 977; 1012pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
nucleotide sequence selected from any of 948 sequences (AB21119-
CC AB21066) or their mature protein coding portion, active domain coding
protein or complementary sequences. The polynucleotides are useful for

CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP6949) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 1805 AA;
Query Match 58.0%; Score 1063; DB 5; Length 1805;
Best Local Similarity 60.1%; Pred. No. 6,4e-95;
Matches 212; Conservative 62; Mismatches 69; Indels 10; Gaps 5;
QY 7 IKVAVRVRPMNRRELDRGAKCIYRMENGTITLTPPGAEEKARKSKTMDGPKAFAPR 66
DB 6 VKAAVAVRPMNRRELNTKCVEMEGNQTVLHPPSNTKQGERK-----PKVFAFDY 59
QY 67 SYWSPDK-NAPNYARQEDLFODLGVPLDPAFKGVNNCIFAYGQTSGSKSYMMGYGKEH 125
DB 60 CFWSMDESNTTKYAGQEVVFKLGGEGILEKAFQGVNACIFAYGQTSGSKSFMMGHAEQL 119
QY 126 GVLPRIQDMFRINLEQDKNLTCTVEVSYLEIYNERVRLDLP-STKGNLKVREHPST 184
DB 120 GLIPRLCALFKRIS-LEQNESQTFKVEVSYMEIYNEKVRDLDPKGRSLKVREHKVL 178
QY 185 GPVEDLAKLVRSFOEINLMDGNKARTVAATNNNETSSRSHAVFTLLTQKMHDEET 244
DB 179 GPYVDLSQLAVTSFEDISLMSSEGNKSRVAATNNBESSRSHAFNIIITQTLVDLOS 238
QY 245 KMDTEKVAKISLVDLGSRATSTGATGARLKEGABINRSLSTLGRVIALADMMSSGKOK 304
DB 239 GNSGEKYSKSVSLVDLAGSERVSKTGAAGERLKEGNSINKSLTTLGLVYISLADQAGK-G 297
QY 305 KQQLVYPRDSVLTWLTLDKSLGNSMTAMTAISPADINFEETLSTLRVADSAR 357
DB 298 KSKFVYPRDSVLTWLTLDKSLGNSQTSMTATISPADNVEETLSTLRVADRAK 350
RESULT 25
ABB62962
ID ABB62962 standard; protein; 1921 AA.
XX
AC ABB62962;
XX
DT 26-MAR-2002 (first entry)
DE Drosophila melanogaster polypeptide SEQ ID NO 15678.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR MPI; 2001-656860/75.

DR N-PSDB; ABL07065.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from *Drosophila* and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 XX Disclosure; SEQ ID NO 15678; 21pp + Sequence Listing; English.
 PS
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (AB557737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from Wipo.int/ftp/pub/published_sequences
 CC
 XX
 SQ Sequence 1921 AA;
 Query Match 56.1%; Score 1028; DB 4; Length 1921;
 Best Local Similarity 60.3%; Pred. No. 2.1e-91;
 Matches 213; Conservative 45; Mismatches 85; Indels 10; Gaps 4;
 QY 7 IKVAVVPPFNAREIDRGAKCIVRMGNTILTPPGAEERKARKSGKTIWDGPKAFADR 66
 DB 6 IKAVAVRPFRNREIELDTKCIEMEQOTILQNPPELEIKERK-----PKTAFDH 58
 QY 67 STWSFPMKAPNVARQEDFDODLGVPLLDNAFKYNNICIFAYGSGSKYSMMGCKEKG 126
 DB 59 CFYSLNPEDENFASOETVFCVGRGLDNAFQGYNCIFAYGSGSKYSMMGCKESKG 118
 QY 127 VTPRICQDMFRRIINELQKQKNTCTVEVSLEYETYNRVRDLNPS--TKGTLKTRHPSTG 185
 DB 119 IIPRLDQLESAIAN-KSTPELMYKVEVSWEIYNEVHDLDPKPKOSLKRHNWVG 177
 QY 186 PYVEDLAKLVRSFOEIEIMDEGNARFVAATNNMETSSRSRAVFTLLTQKHDEETK 245
 DB 178 PVDGSLQALVNSYQDIDNLMTEGNSRTVAATNMAESSRSRAVSVLTQLTLQDNG 237
 QY 246 MOTEKAKISLVDLASERATSTGATGARLKGAETNRSLSLTGRVIALADMSGKQKK 305
 DB 238 VSGEKKVSRMSLVDLASERAVKTAAGVGDRLKEGSINIKSLTTLGLVISKLADQSGKSG 297
 QY 306 N-OLVYRPSVLTWLKDSLGKSMTAMTAISPAINFEETLSTRYVDSAK 357
 DB 298 NDKFVYRDSVLTWLKDLNDGNSRTVWVAITSPSADNTEETLSTLYADRAK 350
 RESULT 26
 AAU19569
 ID AAU19569 standard; protein; 757 AA.
 AC AAU19569,
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Human diagnostic and therapeutic polypeptide (DITHP) #155.
 XX
 KM Human; receptor; diagnostic; therapeutic; gene therapy; vaccine;
 KM cell proliferative disorder; Crohn's disease; lymphoma; leukaemia;
 KM acquired immune deficiency syndrome; AIDS; autoimmune disorder;
 KM respiratory disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200162927-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 21-FEB-2001; 2001WO-US060659.
 XX

PR 24-FEB-2000; 2000US-0184693P.
 PR 24-FEB-2000; 2000US-0184697P.
 PR 24-FEB-2000; 2000US-0184698P.
 PR 24-FEB-2000; 2000US-0184768P.
 PR 24-FEB-2000; 2000US-0184769P.
 PR 24-FEB-2000; 2000US-0184770P.
 PR 24-FEB-2000; 2000US-0184771P.
 PR 24-FEB-2000; 2000US-0184772P.
 PR 24-FEB-2000; 2000US-0184773P.
 PR 24-FEB-2000; 2000US-0184774P.
 PR 24-FEB-2000; 2000US-0184776P.
 PR 24-FEB-2000; 2000US-0184777P.
 PR 24-FEB-2000; 2000US-0184779P.
 PR 24-FEB-2000; 2000US-0184813P.
 PR 24-FEB-2000; 2000US-0184837P.
 PR 24-FEB-2000; 2000US-0184841P.
 PR 24-FEB-2000; 2000US-0185213P.
 PR 24-FEB-2000; 2000US-0185216P.
 PR 12-MAY-2000; 2000US-0203785P.
 PR 15-MAY-2000; 2000US-0204226P.
 PR 16-MAY-2000; 2000US-0204525P.
 PR 16-MAY-2000; 2000US-0204821P.
 PR 16-MAY-2000; 2000US-0204908P.
 PR 16-MAY-2000; 2000US-0205232P.
 PR 17-MAY-2000; 2000US-0204815P.
 PR 17-MAY-2000; 2000US-0204863P.
 PR 17-MAY-2000; 2000US-0205221P.
 PR 17-MAY-2000; 2000US-0205285P.
 PR 17-MAY-2000; 2000US-0205286P.
 PR 17-MAY-2000; 2000US-0205287P.
 PR 17-MAY-2000; 2000US-0205327P.
 PR 17-MAY-2000; 2000US-0205324P.
 XX
 XX (INCYTE GENOMICS INC.
 XX
 XX Panzer SR, Spiro PA, Banville SC, Shah P, Chalup MS, Chang SC,
 PI Chen A, D'sa SA, Amshay S, Dahl CR, Dam TC, Daniels SE, Dufour GE,
 PI Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL, Liu TF,
 PI Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daffo A,
 PI Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W,
 PI Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;
 XX
 XX WPI: 2001-502867/55.
 DR N-PSDB; AAS31140.
 PT
 PT Polynucleotides encoding diagnostic and therapeutic proteins, e.g.
 XX enzymes, hormones and receptors, useful in diagnostics and therapeutics.
 XX
 PS Claim 27; Page 488-490; 522pp; English.
 XX
 CC The invention relates to polynucleotides (I) encoding diagnostic and
 CC therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and
 CC proteins involved in growth and development and receptors (I) and (II)
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate DITHP expression. For example, (I) and (II)
 CC may be used to treat disorders associated with decreased polypeptide
 CC expression by rectifying mutations or deletions in a patient's genome,
 CC that affect the activity of the DITHPs, by expressing inactive proteins
 CC or supplementing the patient's own production of them (I) and (II) may
 CC be used to treat diseases, for example, cell proliferative disorder,
 CC Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma,
 CC leukaemia, autoimmune disorders, and respiratory disorders. Additionally,
 CC (II) may be used to produce the DITHPs, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the protein. (I) and
 CC its complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids in
 CC samples, and therefore which patients may be in need of restorative
 CC therapy. (II) may also be used as antigens in the production of
 CC antibodies against DITHPs and in assays to identify modulators of DITHP
 CC expression and activity. The anti-DITHP antibodies and antagonists may
 CC also be used to down regulate expression and activity. The anti-DITHP
 CC antibodies may also be used as diagnostic agents for detecting the
 CC presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay

CC (ELISA). AAU19415-AAU19625 represent human diagnostic and therapeutic
CC (DITHP) polypeptides of the invention
XX Sequence 757 AA;
Query Match 56.0%; Score 1027.5; DB 4; Length 757;
Best Local Similarity 59.1%; Pred. No. 5,1e-92;
Matches 212; Conservative 50; Mismatches 84; Indels 13; Gaps 6;
QY 3 GGGNKKVAVRPPNAREIDRGAKCIYRMENQITLTPPGAEBKARKSKITMDGPKAF 62
DB 17 GDSKVVAVRIRPMNRRETDLTHTKCVVDANKVILNPNTNLISKDARGQ-----PKVF 71
QY 63 AFDRSYWSFDKNA-PNVARQEDLFQDLGVPLLDNAFQVNNCI PAYGQTSKSKSYMMGY 121
DB 72 AYDHCWSDHDESKYKAGDVIYFKLIGENILONAFGNACIFAYGQTSKSKSYMMGT 131
QY 122 GKEGVIPRICQDMFRINELQDKN--LTCTVEVSYLEIYNERVVDLNP-STKGNLKY 178
DB 132 AADPGIIPRLCSGLFER---TQKEENEGSPKVEVSYMEIYNEKVDLDPKSGRQTLKY 188
QY 179 REHPSTGPIYVEDLAKLVNSFOEINMDGNKARTYAATNMETSRSRSHAVTTLITQK 238
DB 189 REHSVVGPIYVDGLSKLAVTSYKDIESIEMSEKNSRTVAATNMEESSRSRSHAVFKITLTH 248
QY 239 WHDEETKMDTEKVAKISLVNLAGSERATSGATGARLKEGAELNRSISTLGRVIALADM 238
DB 249 LIDVKSCTGSEKRGKSLVDLAGSERATKGAAGDRKESNSINKSLTTLGLVISALADQ 308
QY 299 SSGGQKKNQLVPRYDSVLTWLDKSLGNSMTAMIAISPADINFETTLSTRVADSAK 357
DB 309 SAKK-NKNKRVPRDSVLTWLDKSLGNSKTMAMVATVSPAANNYDETTLSTRVADRAK 366
RESULT 27
ID ABP51294 standard; protein; 757 AA.
XX ABP51294;
AC ABP51294;
XX 03-SEP-2002 (first entry)
XX Human MDT SEQ ID NO 316.
DE Human MDT
XX Human: MDDT, disease detection and treatment molecule polynucleotide;
KW proliferative disorder; hepatitis; psoriasis; cancer; AIDS;
KW autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis;
KW rheumatoid arthritis; transgenic; gene therapy; antiretroviral;
KW hepatotropic; antiinflammatory; antiproliferative; cytostatic; anti-HIV;
KW antiallergic; antianemic; antisthmatic; antiatherosclerotic; antigenic;
KW neuroprotective; antineumatic; antidiabetic.
XX Homo sapiens.
OS Homo sapiens.
PN WO200240715-A2.
XX 23-MAY-2002.
PD 06-SEP-2001; 2001WO-US027628.
XX 05-SEP-2000; 2000US-0229747P.
XX 05-SEP-2000; 2000US-0229748P.
XX 05-SEP-2000; 2000US-0229749P.
XX 05-SEP-2000; 2000US-0229750P.
XX 05-SEP-2000; 2000US-0229751P.
XX 05-SEP-2000; 2000US-0230583P.
XX 06-SEP-2000; 2000US-0230585P.
XX 06-SEP-2000; 2000US-0230514P.
XX 06-SEP-2000; 2000US-0230515P.
XX 06-SEP-2000; 2000US-0230517P.
XX 06-SEP-2000; 2000US-0230518P.
XX 06-SEP-2000; 2000US-0230519P.
XX 06-SEP-2000; 2000US-0230595P.

PR 06-SEP-2000; 2000US-0230597P.
PR 06-SEP-2000; 2000US-0230598P.
PR 06-SEP-2000; 2000US-0230599P.
PR 06-SEP-2000; 2000US-0230610P.
PR 06-SEP-2000; 2000US-0230611P.
PR 06-SEP-2000; 2000US-0230612P.
PR 06-SEP-2000; 2000US-0230613P.
PR 06-SEP-2000; 2000US-0230614P.
PR 06-SEP-2000; 2000US-0230615P.
PR 06-SEP-2000; 2000US-0230616P.
PR 06-SEP-2000; 2000US-0230617P.
PR 06-SEP-2000; 2000US-0230618P.
PR 06-SEP-2000; 2000US-0230619P.
PR 06-SEP-2000; 2000US-0230620P.
PR 06-SEP-2000; 2000US-0230621P.
PR 06-SEP-2000; 2000US-0230622P.
PR 06-SEP-2000; 2000US-0230623P.
PR 06-SEP-2000; 2000US-0230624P.
PR 06-SEP-2000; 2000US-0230625P.
PR 06-SEP-2000; 2000US-0230626P.
PR 06-SEP-2000; 2000US-0230627P.
PR 06-SEP-2000; 2000US-0230628P.
PR 06-SEP-2000; 2000US-0230629P.
PR 06-SEP-2000; 2000US-0230630P.
PR 06-SEP-2000; 2000US-0230631P.
PR 06-SEP-2000; 2000US-0230632P.
PR 06-SEP-2000; 2000US-0230633P.
PR 06-SEP-2000; 2000US-0230634P.
PR 06-SEP-2000; 2000US-0230635P.
PR 06-SEP-2000; 2000US-0230636P.
PR 06-SEP-2000; 2000US-0230637P.
PR 06-SEP-2000; 2000US-0230638P.
PR 06-SEP-2000; 2000US-0230639P.
PR 06-SEP-2000; 2000US-0230640P.
PR 06-SEP-2000; 2000US-0230641P.
PR 06-SEP-2000; 2000US-0230642P.
PR 06-SEP-2000; 2000US-0230643P.
PR 06-SEP-2000; 2000US-0230644P.
PR 06-SEP-2000; 2000US-0230645P.
PR 06-SEP-2000; 2000US-0230646P.
PR 06-SEP-2000; 2000US-0230647P.
PR 06-SEP-2000; 2000US-0230648P.
PR 06-SEP-2000; 2000US-0230649P.
PR 06-SEP-2000; 2000US-0230650P.
PR 06-SEP-2000; 2000US-0230651P.
PR 06-SEP-2000; 2000US-0230652P.
PR 06-SEP-2000; 2000US-0230653P.
PR 06-SEP-2000; 2000US-0230654P.
PR 06-SEP-2000; 2000US-0230655P.
PR 06-SEP-2000; 2000US-0230656P.
PR 06-SEP-2000; 2000US-0230657P.
PR 06-SEP-2000; 2000US-0230658P.
PR 06-SEP-2000; 2000US-0230659P.
PR 06-SEP-2000; 2000US-0230660P.
PR 06-SEP-2000; 2000US-0230661P.
PR 06-SEP-2000; 2000US-0230662P.
PR 06-SEP-2000; 2000US-0230663P.
PR 06-SEP-2000; 2000US-0230664P.
PR 06-SEP-2000; 2000US-0230665P.
PR 06-SEP-2000; 2000US-0230666P.
PR 06-SEP-2000; 2000US-0230667P.
PR 06-SEP-2000; 2000US-0230668P.
PR 06-SEP-2000; 2000US-0230669P.
PR 06-SEP-2000; 2000US-0230670P.
PR 06-SEP-2000; 2000US-0230671P.
PR 06-SEP-2000; 2000US-0230672P.
PR 06-SEP-2000; 2000US-0230673P.
PR 06-SEP-2000; 2000US-0230674P.
PR 06-SEP-2000; 2000US-0230675P.
PR 06-SEP-2000; 2000US-0230676P.
PR 06-SEP-2000; 2000US-0230677P.
PR 06-SEP-2000; 2000US-0230678P.
PR 06-SEP-2000; 2000US-0230679P.
PR 06-SEP-2000; 2000US-0230680P.
PR 06-SEP-2000; 2000US-0230681P.
PR 06-SEP-2000; 2000US-0230682P.
PR 06-SEP-2000; 2000US-0230683P.
PR 06-SEP-2000; 2000US-0230684P.
PR 06-SEP-2000; 2000US-0230685P.
PR 06-SEP-2000; 2000US-0230686P.
PR 06-SEP-2000; 2000US-0230687P.
PR 06-SEP-2000; 2000US-0230688P.
PR 06-SEP-2000; 2000US-0230689P.
PR 06-SEP-2000; 2000US-0230690P.
PR 06-SEP-2000; 2000US-0230691P.
PR 06-SEP-2000; 2000US-0230692P.
PR 06-SEP-2000; 2000US-0230693P.
PR 06-SEP-2000; 2000US-0230694P.
PR 06-SEP-2000; 2000US-0230695P.
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PR 06-SEP-2000; 2000US-0230896P.
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PR 06-SEP-2000; 2000US-0230937P.
PR 06-SEP-2000; 2000US-0230938P.
PR 06-SEP-2000; 2000US-0230939P.
PR 06-SEP-2000; 2000US-0230940P.
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Qy 122 GKEHGVIPIRCODMERRINELQDKN--LTCTVEVSYLEIYNERVDDLNP-STKGNLKV 178
Db 132 ADQPGILPRLCGGLPER---TQKEENEOSFKVEVSymeIYNEKVRDLDPGKSQTCLKV 188
Qy 179 REHPSTGPVEDLAKLVRSFOEINLMDGNKARTVAATNNETSRSRSHAVFTLTJQK 238
Db 189 REHVSIGPVVDGSLKLAVTSYKDIESLMBEGNKSRTVAATNNESRSRSHAVFKITLTHT 248
Qy 239 WHDETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIALADM 298
Db 249 LYDVKSGTSGEKVGKLSLVDLAGSERATYTGAGDRLKEGGSINIKSLTTLGLVIALADQ 308
Qy 299 SSGKOKKQNLVPRDSVLTWMLKDSLGGNSMTAMIAISPADINEEFTLSTLRVADSAK 357
Db 309 SAGK-NKMKFVPRDSVLTWMLKDSLGGNSKTMVAATVSPADNYDETTLSTLRVADRAK 366
RESULT 28
ID ABG60124 standard; protein; 762 AA.
XX ABG60124;
AC
XX
XX
DT 30-JUL-2002 (first entry)
XX
DE Human DITHP polypeptide #182.
XX
XX Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin;
XX cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
XX inflammatory disorder; viral infection; bacterial infection; seizure;
XX fungal infection; parasitic infections; developmental disorder; breast;
XX endocrine disorder; metabolic disorder; neurological disorder; cervix;
XX gastrointestinal disorder; transport disorder; gene therapy; kidney;
XX adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
XX thymus.
XX
OS Homo sapiens.
XX
XX WO200220754-A2.
XX
XX
PD 14-MAR-2002.
PF 29-AUG-2001; 2001WO-US027127.
XX
XX 05-SEP-2000; 2000US-0229747P.
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XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL,
PI Jones AL, Yu JY, Wright RO, Gietzen D, Liu TF, Yap PE, Dahl CR;

PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
PI Gerstein EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
PI Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
DR WPI, 2002-383054/41.
XX N-PSDB; ABK71715.
XX
XX An isolated polynucleotide useful in diagnostics and therapeutics.
PS Claim 29; Page 637-639; 686pp; English.
XX
XX The invention relates to human diagnostic and therapeutic (dithp)
XX polynucleotides and their associated polypeptides (DITHP polypeptides).
XX The sequences of the invention are used in the treatment and diagnosis of
XX cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
XX (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
XX cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
XX thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
XX psoriasis, osteoporosis), viral infections, bacterial infections, fungal
XX infections, parasitic infections, developmental disorders (e.g. anaemia,
XX epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
XX endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
XX (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
XX amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
XX disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
XX (e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences
XX ABG59943-ABG60220 represent human DITHP polypeptides of the invention
XX
SQ Sequence 762 AA;
Query Match 55.6%; Score 1020.5; DB 5; Length 762;
Best Local Similarity 58.8%; Pred. No. 2.6e-91;
Matches 211; Conservative 50; Mismatches 85; Indels 13; Gaps 6;
Qy 3 GGGNKKVYVRVPPFARIEDRGACIVMEGQITLTTPPAEERAKRSKTIYMPRAF 62
Db 17 GDSKVVAVRIRPMMRRRTDLTKCVVDVANKVILNPVNTLSKGDARGQ----PKVF 71
Qy 63 AFDRSYWSFDKVA-DNYARQEDLPQDLGVPLDANFKGNNCTIFAYGQTSGSKSYMMGY 121
Db 72 AYDHCFSWSDSESVKRYAGODIVFKCLGENIILQNAFDGVNACIFAYGQTSGSKSYTMGCT 131
Qy 122 GKEHGVIPIRCODMERRINELQDKN--LTCTVEVSYLEIYNERVDDLNP-STKGNLKV 178
Db 132 ADQPGILPRLCGGLPER---TQKEENEOSFKVEVSymeIYNEKVRDLDPGKSQTCLKV 188
Qy 179 REHPSTGPVEDLAKLVRSFOEINLMDGNKARTVAATNNETSRSRSHAVFTLTJQK 238
Db 189 REHVSIGPVVDGSLKLAVTSYKDIESLMBEGNKSRTVAATNNESRSRSHAVFKITLTHT 248
Qy 239 WHDETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSLSTLGRVIALADM 298
Db 249 LYDVKSGTSGEKVGKLSLVDLAGSERATYTGAGDRLKEGGSINIKSLTTLGLVIALADQ 308
Qy 299 SSGKOKKQNLVPRDSVLTWMLKDSLGGNSMTAMIAISPADINEEFTLSTLRVADSAK 357
Db 309 SAGK-NKMKFVPRDSVLTWMLKDSLGGNSKTMVAATVSPADNYDETTLSTLRVADRAK 366
RESULT 29
ADJ69671
ID ADJ69671 standard; protein; 1826 AA.
XX
XX ADJ69671;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human heat mitochondrial protein as a therapeutic target Segid1477.
DE
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
XX Huntington's disease; osteoarthritis;
XX Leber's hereditary optic neuropathy; LHON;
XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW	myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW	neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW	osteopathic; ophthalmological; cyostatic.
XX	
OS	Homo sapiens.
XX	
PN	MO2003087768-A2.
PD	
XX	23-OCT-2003.
XX	
PF	04-APR-2003; 2003WO-US010870.
XX	
PR	12-APR-2002; 2002US-0372843P.
PR	17-JUN-2002; 2002US-0389987P.
XX	20-SEP-2002; 2002US-0412418P.
XX	
PA	(MITO-) MITOKOR.
PA	(BUCK-) BUCK INST AGE RES.
PI	
PI	Ghosh SS, Faly ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
XX	Warrock DE;
XX	WPI; 2003-845369/78.
PT	
PT	Identifying a mitochondrial target for drug screening assays and for
PT	treating diseases associated with altered mitochondrial function.
PT	comprises detecting a modified polypeptide in a sample and correlating
PT	with the disease.
XX	
PS	Claim 1; SEQ ID NO 1477; 180pp; English.
XX	
CC	This invention relates to novel mitochondrial targets that can be used
CC	for therapeutic intervention in treating a disease associated with
CC	altered mitochondrial function. Specifically, it refers to a method for
CC	identifying proteins of the human heart mitochondrial proteome that are
CC	useful for drug screening assays, as well as therapeutic targets. The
CC	present invention describes a method for identifying such proteins that
CC	can be used in the treatment of various diseases associated with altered
CC	mitochondrial function including diabetes mellitus, Huntington's disease,
CC	osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC	encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC	ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC	compositions have neuroprotective, nootropic, antidiabetic,
CC	anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC	cyostatic activities. This polypeptide sequence is a human heart
CC	mitochondrial protein of the invention.
XX	
XX	Sequence 1826 AA;
XX	
Query Match	55.4%; Score 1016.5; DB 7; Length 1826;
Best Local Similarity	58.5%; Pred. No. 2.7e-90;
Matches 210; Conservative	49; Mismatches 87; Indels 13; Gaps 6
Yy	3 GGGNKKVVVVRVFPFAAREIDRGAKCIVRREGQOTILTPPGAEBKARKSGKTMDPKAF 62
Db	2 GDSKKVAVNRIRPNMRRETDHTKCVVDVDAKKVILNPVNTULSKODARGQ-----PKCF 56
Qy	63 AFDPSYMSFDKNA-DNYARQEDLPDGLVPLIDNAFKYNNCFPAYGQTSGSKSYSMMGY 121
Db	57 AYDHCFFWMSDESVEKEKYGODIVFCKLGENIILQNAFDFGNACIFAYGQTSGSKSYMMGT 116
Qy	122 GKEHGVIIRICODMRRINLEOKDKN--LTGCVASYLEINVERVADLNP-STKCNLAV 178
Db	117 ADQGPLIRLGLGFLER--TKENESEDSFVSEVSYMEITVEKARDLDPKGSRTLKV 173
Qy	179 REHPSTGTYVEDLAKLVVRSFOEILENLDGKNKARTVAATNNNETSSRSRAVFTLLTOK 238
Db	174 REHSVIGPYVDOLSKLAATSYKDISLSEGNKSRVATANNNESSRSRAVILKITLTH 233
Qy	239 WHDETTRKMDTEVNAKISLVDLAAGSRATSTGATGARKLGCAEINSLSTLGRVIALADM 298
Db	234 LYDAKSGTSGEVEVGLSLVDLAGSRATTTGAAGRLKEGNSINBELTTLGLVISAIDQ 293

OY	299	SSGKQKKNQVLPYRDSVLTWLLKDSLGNSMTWIAAISPADINFEETLSTLRVDSAK	357
Db	294	SAGK-NKKKFPYRDSVLTWLLKDSLGNSKTMVATVSPAADVDETLSTLRVADRAK	351
RESULT 30			
ID	ADL83235		
AC	ADL83235	standard; protein; 1826 AA.	
XX	ADL83235;		
XX			
DT	17-JUN-2004	(first entry)	
XX			
XX	Human PRO60891, SEQ ID 437.		
DE			
XX	Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;		
KW	Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;		
KM	Gene therapy; PRO; B cell related disorder; cancer;		
XX	Immune-mediated inflammatory disease; human.		
OS	Homo sapiens.		
XX			
PN	WO2004024097-A2.		
PD	25-MAR-2004.		
PF	15-SEP-2003; 2003WO-US029097.		
PR	16-SEP-2002; 2002US-0411392P.		
PA	(GETH) GENENTECH INC.		
PI	Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WJ;		
PI	Mu TD;		
XX	WPI; 2004-329389/30.		
DR	N-PSDB; ADL83234.		
XX			
PT	New PRO polypeptide, useful for diagnosing and treating a B cell related		
XX	disorder; e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune		
XX	mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.		
PS	Claim 10; Fig 437; 695pp; English.		
XX			
XX	The present invention relates to PRO proteins and their coding sequences.		
CC	The PRO proteins are useful for diagnosing and treating a B cell related		
CC	disorder, e.g. X-linked infantile hypogammaglobulinemia, polyaccharide		
CC	antigen unresponsiveness, selective IgA deficiency, selective IgM		
CC	deficiency, selective deficiency of IgG subclasses, immunodeficiency with		
CC	hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's		
CC	lymphoma, intermediate lymphoma, follicular lymphoma, type II		
CC	hyperesensitivity, rheumatoid arthritis, autoimmune mediated hemolytic		
CC	anemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or		
CC	ankylosing spondylitis. The PRO proteins are also useful for preparing a		
CC	medicament for treating a condition that is responsive to the PRO		
CC	protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO		
CC	coding sequences are useful as hybridization probes in chromosome and		
CC	gene mapping, in preparing PRO proteins, or in generating transgenic		
CC	animals or knockout animals, which in turn are useful in the development		
CC	and screening of therapeutically useful reagents.		
XX			
SQ	Sequence 1826 AA;		
Query Match	55.4%;	Score 1016.5;	DB 8; Length 1826;
Best Local Similarity	58.5%;	Pred. No. 2,7e-90;	
Matches 210;	Conservative 49;	Mismatches 87;	Indels 13; Gaps 6;
OY	3	GGGNIKVVVVRFPFNAREIDRGAKCIVRMEGNOTILTPPGAEERKRSKGTIMDPKAF	62
Db	2	GDSKVVAIVAIRPMNRREIDLTHTKCVVDVDAKVIINPVVNTLSKGDARQ-----PKCF	56
OY	63	AFDRSYWSFDKNA-PNYARQEDLFDLGLVPLLDNAEKGYNNCIPAYGQTSGSKSYSMWG	121

Db 57 AYDHCFWMSDESVKEXYAGDVIKFCIGENILQNAFDGVNACIFAYGQTGSGKSYTMGT 116
Qy 122 GKEHGVIPRIQDMFRINELQDKA--LTCTVEVSYLEIYNERVRLNP-STKGNLKY 178
Db 117 ADQPGIIPRLCSGLFER--TQKEENBEO\$FKVEVSymeIYNEKVRDLDPKGSROTlKY 173
Qy 179 REHPSGTPIVEDLAKLVNRSFOEIEIENLMBEGNKARTVAATNMNETSSRSHAVFTLTLQK 238
Db 174 REHSVULGPYVDGSLKLAATSYKDIESIMSEGNKSRITVAATNMNEBSSRSHAVLKITLHT 233
Qy 239 WHDEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINRSISTLGRVIAALADM 298
Db 234 LYDAKSGTSGEKYKXLSLVDLAGSERATKTGAAGDRLKEG\$NINESITTLGLVISALADQ 293
Qy 299 SSGKQKKNQLVPRDSVLTWLLKDSLGNSMTMIAAISPADINFEETLSTLRVADS\$K 357
Db 294 SAGK-NKNKFVPRDSVLTWLLKDSLGNSKTMVATVSPADNYDETISTLRVADRAK 351

Search completed: September 5, 2006, 18:04.43
Job time : 201 secs